

ATTTAATAAT CCTTTGTTAC CTGTGAATGA AGGAACTTTG TAATTCTGAT TTATCGTAAA 540  
 ACATGAGCCT TTCCAGAGTC AGCTTAGACA CTGTTGTCGC AAATAGCCAT GCTTTGCCTT 600  
 5 ATGCCAAGGA GGGCCAGAGG GAGGGCCTAG TCTTCCTCTG TTGCTGTACA TATATTGAAA 660  
 TGCTTTTTTT TTTTATTTTG CATTTGTTAT CTATAATGAG CTTTCTGAGC CCTGATATTA 720  
 10 TGTGAGACAA ACAGGAGTTA TTGATGTTAT ACACTCCCTT CCATTCAGGA TTTTCTGCTT 780  
 GGAGGGAAAT ATGTTGACCT TAGAGAATTG TGAATATTGT TGCAATTCTT GAATATATTA 840  
 CCATGTGAAT AATAGAGACT GTGTTGCTCT CTAGTATAAG CTATATTTAT TTTTGATTCA 900  
 15 TTTGAATTAC TAGTTATAAC TGGAGAAATT TTGTTACCTC TATCCTGGCT TGCCTGACTG 960  
 GCTGTATAAT AGCAGCAGCC TCTTTTAGAG CATCTTAATG AAAACATGGA TGAAGGAAT 1020  
 20 TAATGATGAT ATCTGCAGAC TGGGTAGAAA ATGGCTTTTG TTCCCGCGT TAACATTTTC 1080  
 TTCTCAATCA CATTTCAATG TTTGTGGAGA GTGGCAGATT CACACCAGAA ACACTAGGTG 1140  
 TTCATATCCA TAGCATGGAT GCAGAATAAG CAGTTGGGAG AGAAGCTTCT TCCTACCTGG 1200  
 25 TACTCCTCCC ATTCACCTCA GCCCAGCCCC AGACAGGCGT TAGCATTCAG TGTGGGCCCT 1260  
 CAGGCAGCCC TGAAGCCTGG CTGGTCAATC AGATGGGGGC AGCCTGTGAC GGGCACCAGC 1320  
 30 GGCTGATTTC CAGGGAAGAG TTCTGGAGG GTGTTGGCTG TTTTGTAG CTCAGTTTTT 1380  
 TTCTGGGCTC CACCATTCTT AACTCCAGGT AGACAAGATA GATGTCACAC ACAAGAATT 1440  
 TAAAGTATTT TGCTTAGTGC ATTTTGTTTA TGATTGCAGT GTTTGTTTCT TATTTAATAG 1500  
 35 GCTTTTACT TCATTCTATT AAATTTAGT GTTTAGAAGA GGCGGGTACT GTCAGTGTG 1560  
 AAAATATGTA ATATTTTATA TGTATACCA TGTATATAT ACTTGCAATA TCAGACCTTG 1620  
 40 CATTCATAT ACAATGCAAT TGAATCTTTG CAGACCTGCA TTTTTCAGTG AACATAAAA 1680  
 AGATTGTCTG GCACTCCAAA AAAAAAAAAA AAAAAAAAAA 1720

45

(2) INFORMATION FOR SEQ ID NO: 134:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 705 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

GGCACGAGGC CATCTGGGCT CATTCAGCAG GAAATAATGG AAAAGCTGC AATATCCAGG 60  
 TGTTTACTAC AATCTGGAGG CAAGATCTTT CTCAGTATG TGCTGATGTT TGGGTGCTT 120  
 60

386

GTGGAATCAC AGACACTCCT AGAGGAGAAT GCTGTTCAAG GAACAGAACG TACTCTTGGA 180  
 TTAAATATAG CACCTTTTAT TAACCAGTTT CAGGTACCTA TACGTGTATT TTTGGACCTA 240  
 5 TCCTCATTCG CCTGTATACC TTTAAGCAAG CCAGTGGAAC TCTTAAGACT AGATTTAATG 300  
 ACTCCGTATT TGAACACCTC TAACAGAGAA GTAAAGGTAT ACGTTTGTNA AATCTGGGAA 360  
 10 GACTTGACTG CTATTCCATT TTGGGTATCA TATGTACCTT GATGAAGANG ATTAGGTTGG 420  
 GATACTTCAA GTGAAGCCTC CCACTGGAAA CAAGCTGCAG TTGTTTTAGA TAATCCCATC 480  
 CAGGTTGAAA TGGGAGAGGA ACTTGTAATC AGCATTTCAGC ATCACAAGAG CAATGTCAGC 540  
 15 ATCAGAGTAA AGCAATGAAG AGCAGTTTTT CAATGAAAAC TGTGTAAATA GAGCATCAAC 600  
 AAGTACAAA TTCTTGCTTT AATTAGTGGG GGTATATAAA AATTCCTTGT AATGOTCAA 660  
 20 TATTTTTTAA AATTGACATT AATAAAGCAT ATTTTAAAAG TTTCT 705

25 (2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

35 AGCACACACC TCCTTTAGTT GCTCCTAAGG TCATGTTCAA CATTGCTGGA GTGCATTTTC 60  
 TGCTCAGGGA GCTTTCCAG ACCCGGAATG TTTGGTGCTC ACAGACYCTG GCAAGGATCG 120  
 GTATTGCTGT TCCTCAGTTT TGCCTGGGGA AATGGAGGST CAGTGACGTT CAGTGACGTG 180  
 40 CCCAGAGTCA TGCCATTGGC GGSTGGCCCA GKGMTCCAGG TCTCCAGCAC CCTCGGCCCC 240  
 CCTCCTCACC AGGTACATC ATCTCCTGGA TTAGAATCTG CTCACATAGT CTGTCTCGAA 300  
 45 AGGAAAAAAA AAAAAAAAAA AAC 323

50 (2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 582 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

60 GGACGGAATG GTGCAACCCT CCTWAMTTTT CTKGKCTGT TGACACAGA GGGAGGGAGG 60



5 GAAAACATTT TTYGTGGGAG AATCCTACYT CTGCAGSGGA GGCCTTAAGC GATKGMTTTT 120  
 GAATCTKGAC CCTTTACCAA CTAATTTTGA AGGAAGATAC CTTGGAPATA TTTGGCATTG 180  
 10 AGTGGGTTAC TGAACAGCA TTAGTGAATT CATCTAGAGA ACTCTTTCAT TTATTCAGGC 240  
 AACAACTGTA CAACCTGGAA ACCTTGTTAC AGTCCAGTTG TGATTTTGGG AARCTATCAA 300  
 CTCTACACTG CAAAGCAGAC AATATTAGGC AGCAGTGTGT ACTATTTCTC CATATGTGA 360  
 AAGTTTTTCAT CTTGAGGTAT CTGAAAGTAC AGAATGCTGA GAGTCATGTT CCTGTCCATC 420  
 CTTATGAGGC TTTGGAGGCT CAGCTTCCCT CAGTGTGAT TGATGAGCTT CATGGATTAC 480  
 15 TCTGTATAT TGGACACCTA TCTGAACCTC CCAGTGTAA TATAGGAGCA TTTGTAAATC 540  
 AAAACCAGAT TAAGGTTTGA CTGGTTTCAT TTGATTTTGA AG 582

20

(2) INFORMATION FOR SEQ ID NO: 137:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1021 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

TTGGGCAGAG CCCTTGGCGG CTCTTGAATA CCTGCKTTCT GTAGCGCTAG TTCTCTTCAA 60  
 GATTTGCTTA GTGTCAATTC ATTTGGGTTT CTTTTCTCGC CATGTTTTTC TGTGGGAATT 120  
 35 ACGGTTTCGT TTGTTCTAT GACTCTCTA AAATGTTATC GTTTTTCATT TGTCTACTAA 180  
 TTTTGTGCA TTTGTTACTA CTGAGTTTCT TAATATCTGA CTGGCCTCCG CCCACGGGCT 240  
 40 CTGCAGANCA TAAAATACTC AGGCTGATGG TAGTGCAGAG ACTCTCCCTC CTTGATCAGC 300  
 GCAAACGTTG GTCTGAGGCT TGAGGGATGG AGCAACATTT TCTTGCTGT GTGAACCGGG 360  
 CTTGGGATTC CGCAGAGGTG GGGCCAGAGC CCCAGCCTCC ACCTATTGTG AGTTCAGAAG 420  
 45 ATCGTGGGCC GTGGCCTCTT CTTTGTATC CAGTACTAGG AGAGTACTCA CTGGACAGCT 480  
 GTGATTTGGG ACTGCTTTCC AGCCCTTGCT GGCGGCTGCC CGGAGTCTAC TGGCAAAACG 540  
 50 GACTCTCTCC TGGAGTCCAG AGCACCTTGG AACCAAGTAC AGCGAAGCCC ACTGAGTTCA 600  
 GTTGGCCGGG GACACAGAAG CAGCAAGARG CACCCGTAGA AKAAGTGGGG CAGGCAGARG 660  
 AACCCGACAG ACTCAGGCTC CRGCAGCTTC CCTGGAGCAG TCCTCTCCAT CTTTGGGACA 720  
 55 GACAGCAGGA CACCGAGGTC TGTGACAGCC GGTGCCTTTT GGAACGCCGC CATCCTCCTG 780  
 CCCTCCAGCC GTGGCCGCAC CTCCCGGTT TCTCAGACTG CCTGGAGTGG ATTCTTCGGC 840  
 60 TTGGTTTTCG CGGTTTCTCT GACTCTGGG CGTCTGTTT ACAGGATCTGT GGAGCTAAGC 900

AGCCTTAGAT AGCAGCAGAA GGCCTTTTGG ATTCTCCTCC TTGAAAAGAT TCTCAGTTAC 960  
 CAAACGTCTC CACCTAGAAA ATAAAAATAC ATTAAGATGT TGANAAAAAA AANAAAAAAA 1020  
 A 1021

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CGGAAGATGA TGGCTTCAAC AGATCCATTG ATGAAGTGAT ACTAAAAAT ATTACTTGGT 60  
 ATTGAGAAG AGTTTAACT GAAATCTCCT TGGGGAGTCT CCTGATCCTG GTGGTAATAA 120  
 GAACCATTCA ATACAACATG ACTAGGACAC GAGACAAGTA CTTTCACACA AATTGTTTGG 180  
 CAGCTTTAGC AAATATGTCG GCACAGTTTC GTTCTCTCCA TCAGTATGCT GCCCAGAGGA 240  
 TCATCAGTTT ATTTTCTTTG CTGTCTAAAA AACACAACRA AGTTCTGGAA CAAGCCACAC 300  
 AGTCCTTGAG AGGTTGCTG AGTTCTAATG ATGTTCTCTT ACCAGATTAT GCACAAGACC 360  
 TAAATGTCAT TGAAGAAGTG ATTCGAATGA TGTTAGAGAT CATCAACTCC TGCCTGACAA 420  
 ATTCCCTTCA CCACAACCCA AACTTGGTAT ACGCCCTGCT TTACAAACGC GATCTCTTTG 480  
 AACAATTTG AACTCATCCT TCATTTCAGG ATATAATGCA AAATATTGAT CTGGTGATCT 540  
 CCTTCTTTAG CTCAAGGTTG CTGCAAGCTG GGAGCTGAGC TGTCAAGTGA ACGGGTCTG 600  
 GAAATCATTG AGCAAGGCGT CGTTGCGCTG CCCAAAGACA GACTGAAGAA ATTTCCAGAA 660  
 TTGAAATTCA AATATGTGGA AGAGGAGCAG CCCGAGGAGT TTTTATCCC CTATGTCTGG 720  
 TCTCTTGTCT ACAACTCAGC AGTCGGCCTG TACTGGAATC CACAGGACAT CCAGCTGTTT 780  
 ACCATGGATT CCGACTGAGG GCAGGATGCT CTCCCACCCG GACCCCTCCA GCCAAGCAGC 840  
 CCTTCAAGTT CTTTTATTTC TGGTAAACAG AAGTAGACAG ACAGGTTACT TGGTGTATCT 900  
 TCTGTAAAG AGGATTGCAC GAGTGTGTTT TCCTCACACA CTTTGATTG GAGAATTGGT 960  
 GCTAGTTGGC AATAGATAAC TCAGCGTAGA TAGTATTGCA AAAAGGGGAG GAAATACACA 1020  
 ACAATAATAA ATGTAAAAAC CTGCTATTCA ACATGCAGTT TTATTTGCGAR GCCAAAAATC 1080  
 TAGAGCTTTC CCAAGATCCT GTTGCCTTAG GCACATNCAC ACTTCAACAG TGCACTAT 1140  
 CCAACAGTGC ACACTATTCA AAGTGCACA CTATTCAAAA GCGTAGACTA TTTTTTTGCA 1200

TGTTCAGAT ATTTGTTTTG GTCTTATGTG TGTGTGAGAG AGAGAGATTC CTTTGACATT 1260  
 AAGGAGCATC AATGAGAAA GATGATGAGG CAGGAATTAA TAAAGAAATG AAGTCGTGTG 1320  
 5 TGTTTGGTTG CCTGTGAGAG GGCACACAAT TTCATAAACA CCATGCCCTGG ACPATTTGAT 1380  
 ATTAATATTT AACACCTCTG CATCTTTTTC TTAAAAAAGA ATATGGGCCA GATACAGTGG 1440  
 CTCACATTTG TAATCCCAGC ACTTTGGGGA GCCAAGTTAG CAGAATCCCT TGAGCACAGG 1500  
 10 AATCTGAAAC CAGCTTGGGC AACATAGTGA GATCCCATCT NTACAAAAA CTTAAAAATT 1560  
 AGCCAGGCAT GATGGCAGAT TCCTGTAGTC CTAGCTACTC AGGAGGCTAA GGTAGGAGGA 1620  
 15 TTGCCTGAGC CCAGGAGTTC AAGGCTGCAG TGAGCTAAGN ACGTGCCAGT ACACTCCAGC 1680  
 CTGAGCCACA AAGTGAGACC CTGTCTCGCA AAAAAAAN TTAAAAAGTC GGGGGGGGGC 1740  
 CCGGTACCCA AATCGCCGGA TATGATCGTA AACRATC 1777  
 20

(2) INFORMATION FOR SEQ ID NO: 139:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

35

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTGGG AATGAGAAA TAACTTTATT 60  
 TTCATTGTGG GGAGCGGGCC GATGTCCAGC CTCAGAACTT CTGGAAGTGC TTCTTGGTGC 120  
 CGGCAGCCTT GGTGACCTTG AGCAGCTTGA AGCGCACTGT CTGCTCAGA GCGCGGCACT 180  
 40 CGCCCACTGT GACGATGTCA CCGATCTGGA CGTCCTTGAA GCAGGGGGAC AGGTGTACAG 240  
 ACATGTTCTT GTGGCGCTTC TCGAAGCGGT TGTACTTGCG GATGTAGTGC AGATAGTCTC 300  
 GGCGGATGAC AATGGTCTTC TGCATCTTCA TTTTGGGTCA CCACGCCAGA GAGGATCCGC 360  
 45 CCTCGAATGG ACACATTACC AGTGAAGGGG CATTTCTTGT CAATGTAGGT GCGCCTCAAT 420  
 AGCCTCCTTG GGGTGTCTTT GAAGCCGAGA CCGATGTTCT TGTAGTAAC CCGCGGGAGC 480  
 50 TTCTCCTTGC CAGTTTCTCC CAGCAGGACC CTCTTCTTGT TTTGAAAGAT GGTCCGGCTGC 540  
 TTTTGGTAGG CACGCTCAGT CTGAATGTCC GCCATCTTCT CGTCCCGAAT TCCTGCAGCC 600  
 55 CCGGGGATCC ACTAGTTCTA GAGCGGCCGC ACCGCGGTGG AGC 643

60

(2) INFORMATION FOR SEQ ID NO: 140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

GGCAGGAGGA TGATAGACCT ACTGGAGGAA TACATGGTTT ACAGGAAGCA TACCTACATR 60  
 AGGCTTGATG GCTCATCCAA GATCTCGGAG AGGCCAGACA TGGTGTCTGA TTTTCAGAAC 120  
 AGGAATGACA TCTTTGTGTT CCTGTTAAGC ACAGGAGCTG GACGACTGGG TATCAATCTC 180  
 ACTGCTGMAG ACACAGTGCA TTTTGTATGA TAGCGACTGG AACCCCACTG TGGACCAGCA 240  
 GGGCATGGAC AGGGCCCACC GCTTAGGGCA GACAAAGCAG GTTACTGTGT ACCGGCTCAT 300  
 CTGTAAAGGC ACCATTGAAG AACCCATTCT GCAAAGAGCC AAGGAGAAGA GTGAGATTCA 360  
 GGGATGGTG ATTTCAGGTG GGAAGTTCAA ACCAGATACC TTGAAACCCA AAGAGGTGGT 420  
 TAGTCTTCTT CTAGACGACG AAGAGTTGGA GAAGAAACGT ATGTACTCTA AACCTCTATA 480  
 CACTCCCCCTC ACGTATCTGA GAATGGAAGA GGTACTTGGG TGTGTGCCAA GGGTTAGGCA 540  
 AAGCCAGAGG CTGTATTTAG GGAAAGTATT TTTGTGCTCA TATTTTATAT AAAAACCCAA 600  
 ACAAGAATGT GTTTGTAGGC CAGGCGTGGT GGTCGCGCC TCTAGTCTCA GCATTTCGGG 660  
 ARGCCAAACT GGGCAGATCA CCTGARGTCA GGARTTTGAG TTTGARACCA GCCTGGCCMA 720  
 CGTTGTGAAA CCCCACCTCT ACTARGARTA CSGAAAATTG GTTGGGCATG GTGGCGGGCA 780  
 CCTGTAATTC CAGCACTTTC GGAGGCTGGG GCAGAAATAT TGCTTGAGCC CAGGAGGTGG 840  
 ACATTGCGGT GAGCCGAGAT YGTGCCATTG CAMTCCAGCC SGGGCAATAA GAGTGAAAYT 900  
 CCATCTTTTA AAAACAAACA AAAACAAAAA ACACAAGACC GCTCACACCT GTAATCCCAG 960  
 CACTTTGGGA RGCCGARGCA GGTGGATCAC GARGTCAGGA GTTCCAAGAC TAGCCTGGCC 1020  
 AACCTGGTGA AGCCCCGTCT CTACTAAAAA TACMAATATT AGTCGGGCGT GGTGGTGGCC 1080  
 ACGTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA TCCCTTGAAG CTAGGAGGCA 1140  
 GAGGTTGCAG TGAGCCAGGA TCGTGCCATT GCACTCCAGC CTGGACAACA AGAGCAAGAT 1200  
 TCCATCTCAA AAAAAAAAAA 1220

## (2) INFORMATION FOR SEQ ID NO: 141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

5 AATTGGGCAC GAGCCAGGTT AGCCGGAAGG GCAGCTCTCC AGGCCCTGCC CACCCACACG 60  
 GGGGCTCCTT ATGCACAGCG GGGCTCTCC TTGTGGCCAT AGAAACGGAA CTGGCTCTTT 120  
 TCAACAGTGC TCCAAGAGGA TGGTTATTTA ACCGTGGCCC CCAAGGAGGA AAGGCACAGA 180  
 10 CTTTCCTCCC TCCTGGAACA TCCAAGGGCA CTGGATCCTC TGTGTCCCTC TGAGATGGGG 240  
 TGCCACTCCA GCAAGAGCAC CACGGTGGCA GCTGAGTCCC AGAAGCTTGA AGAAGAGYGC 300  
 15 GAGGGAAGAG AGCCAGGTCT GGAGACCGGC ACCCAGGCAG CAGACTGCAA GGATGCCCCG 360  
 CTGAAGGATG GAACCCCTGA GCCAAGAGC TGAATGCCT CTCTCCAGAG TCGGACCCCTC 420  
 ACCTCTTCC TGGAACTGCC TTTGGCCCCA GAACCATGAG ACAATCCCA CCCTGAGAAG 480  
 20 CTCCGATCAC TGGGAGGAGA GAGAAAGCCT CCAGCTTTGG GATTCAGCCT TCAGAAGTTT 540  
 TTAGCAGCCT TTGCTCATTG GAGAGGTGGG GAAAGGATAA AGTTCTTATA AGGAAATCCC 600  
 25 TAATTTCCCC CAGCTCCTCC CCNCCNGAAG AAGGAACNAA AGAAAGTTCC TTCCACACGT 660  
 TTTGTTGGAA ACTTTTCCCT TGCCAACCTT CTTGGATTG CCAGAACAAA GCCCTCCAGA 720  
 A 721

30

## (2) INFORMATION FOR SEQ ID NO: 142:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1468 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAATTAAT GTTTATAAAT GACTGTACTG AATTTAAAC CGTACGTTT CATTTGCATT 60  
 45 TTGACATTAC TTTATTATAC ATTTTGCATT TAAAAGGCTG CACCAGTTGG CTTTCTTCT 120  
 GTTTATTCT CAAAATATAG AGATTCTGTG ATTTATTTC CCTGTTTATG GATTAAAAAG 180  
 50 AAAATTCTAA TATAAAGCAT TTCAATAGGA TGCAATAGTA TATTACGTTT TTAAATGCT 240  
 TTAGATCTGT GATTCTTGAC TTAATTTTA TTTTATCCC TTAAAGTCAG GGATGCTTTA 300  
 TTCTATTTTA AAGCACTTAT GAGTTACATG TTGTAATCAA GTTTGCACAA TATATTTATC 360  
 55 TATATGAGGA ACCCTAAAT GAATAGCTAA TTTTAAAT GCCATTAAAA TGCATGAAAT 420  
 KCTTATTTAA ACCTTACTAT ACTATTTCTT CAAGGCAAGT AAATTGACCA TGRGAAAGR 480  
 60 ACACAGTTAT TAAACACTGT TGACAGGAAA ATTCTCCTTG ATAACATAGG ACAATTAATG 540

392

GAAAAAAAAA TTCTCATTAT TTGCAAAGAA TGAACAAGTT AATGAACAAA CAAACTAGAT 600  
 TTGGTATGTT TTCAGCTTTT GTATCATGTT TAATTGTTTA ATTTGGTTGA AAAACTGCAG 660  
 5 TTGAGAAATC AGATAGCAAT ATAGACATTG ACAGCAGCTC TGTGGATACC ATGTAATTGT 720  
 CAGGTAATTT CAGAATGTTG AAAATTATTC AGTGCAGCCC TCATAGTATC ATACTTGAAG 780  
 10 AAATTGATTA CAGTTCCACT AAATTGTTGA AGATAAATTA TTTTAAAGG TTATGAAAAC 840  
 TAAGTTATAT TAATTCATAT GTTTGATTTT TAAATCCCAC CTCCTGAAGC TATCCAAATT 900  
 NCTGACTTTG AAAATAACCA TGAGAGATGC CACATTCTC TCTGGGAAAC TACCCTCAA 960  
 15 AGAATAATG TTAATAATTA ACCTTTTAGG TATTAGAAGC TGTATAAAG TATAAATTA 1020  
 AGATATAAGC AGATCACATG TAAATCATTG CTAAAGCACA AGAAAAGAAT GTGCCTTGAT 1080  
 GTACATATAT TACTAAGTTG CCTCTCCCAG TTTACTTTAA AAATGGCTTT AAGGATAAAG 1140  
 20 AATAAATGTG ATAGCTGTGC ATGCATTATA TATTTGCATT TGCAAATTC CCATTGTTTT 1200  
 AACAGCTGTG TGGCTGACTT TCAATTTTAA GACGTGAATT GACATACAGC CCATAACTTT 1260  
 25 ATAATGGCTG CTCATTTATC TTATCTTTCA GTTAGTGGAA AAACATTTCA ACCTGACTAA 1320  
 AATTGGAAT TGTGTCTTTT ATGTTCCATC CTCTGTGTT ACTAGATTTA GTTTAAAAAT 1380  
 30 TGTGTATGAC CATTAATGTA TGTCAATAAC ATGTAATAA AAGATGTTGA ATCTTGTTGA 1440  
 AAAGCAWRAA AAAAAAAAAA AAACCTGA 1468

35

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

45

TGAATTTTTT GCCAAACTTA GTAACCTCTGT TAAATATTTG GAGGATTTAA AGAACATCCC 60  
 AGTTTGAATT CATTTCAAAC TTTTAAATTT TTTTGTACT ATGTTTGGTT TTATTTTCCT 120  
 50 TCTGTTAATC TTTTGTATTC RCTTATGCTC TCGTACATTG AGTACTTTTA TTCCAAACT 180  
 AGTGGGTTTT CTCTACTGGA AATTTTCAAT AAACCTGTCA TTATTGCTTA CTTTGATTAA 240  
 55 AAAAAAAAAA AAAAAAAAAA AAACCCCNAG GGGGGGGCCG GGTNCCCAAT CCCCCCCAA 300

60

(2) INFORMATION FOR SEQ ID NO: 144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60

TGCCCTCCCTT CCTGCAGATT GTGGACAGTA GTTCCTCAGC CTGCACCCCTG GATTCCTTCT 60  
 TCCCCCTCCT AGCTCCATGG GACTCGCCCC AAGACTGTGG CTTCAAGGAC CACCAGCCCC 120  
 TTACTIONCA AGCCCTGACT GTGGAGTTGG TAGATGCCTC TGATCCTCAG TATTCTCTCT 180  
 GGCAATGTTT CACGGCTTCT CCTTCCTGGG AGCTGGCTCC ATAACCTGAT TTTCCCCAAA 240  
 CGTGTTCGAA TCCCTGCTGC CCCTTAGCCA CCCAGGGTCT TGTGTGGTA TGAGTGTAGA 300  
 GGATGGGGGT ATGCCAGGCC TGGGCCCTCC CAGGCAGGCC CGCTGGACCC TGATGCTACT 360  
 CCTATCCACT GCCATGTACG GTGCCCATGC CCCATTGCTG GCACTGTGCC ATGTGGACGG 420  
 CCGAGTGCCC TTYCGGCCCT CCTCAGCCGT GCTGCTGACT GAGCTGACCA AGCTACTGTT 480  
 ATGCGGCTTC TCCCTTCTGG TAGGCTGGCA AGCATGGCCC CAGGGGCCCC CACCTTGGCG 540  
 CCAGGCTGCT CCCTTCGCAC TATCAGCCCT GCTCTATGGC GCTAACAACA ACCTGGTGAT 600  
 CTATCTTCAG CGTTACATGG ACCCCAGCAC CTACCAGGTG CTGAGTAATC TCAAGATTGG 660  
 AAGCACAGCT GTGCTCTACT GCCTCTGCCT CCGGCACCGC CTCTCTGTGC GTCAGGGGTT 720  
 AGCGCTGCTG CTGCTGATGG CTGCCGGAGC CTGCTATGCA GCAGGGGGCC TTCAAGTTCC 780  
 CGGGAACACC CTTCCAGTC CCCCTCCAGC AGCTGCTGCC AGCCCCATGC CCCTGCATAT 840  
 CACTCCGCTA GGCCTGCTGC TCCTCATCTT GTACTGCCCT ATCTCAGGCT TGTCTCAGT 900  
 GTACACAGAG CTGCTCATGA AGCGACAGNG GCTGCCCCCTG GCACTTCAGA ACCTCTTCCT 960  
 CTACACTTTT GGTGTGCTTC TGAATCTAGG TCTGCATGCT GCGGGGGGCT CTGGCCCAGG 1020  
 SCTCCTGGAA GGTTCCTCAG GATGGGCAGC ACTCGTGGTG CTGAGCCAGG CACTAAATGG 1080  
 ACTGCTCATG TCTGCTGTCA TGAAGCATGG CAGCAGCATC ACACGCTCTT TTGTGGTGTG 1140  
 CTGCTCGCTG GTGGTCAACG CCGTGTCTTC AGCAGTCCTG CTACGGCTGC AGCTCACAGC 1200  
 CGCCTCTTTC CTGGCCACAT TGCTCATTTG CCTGGCCATG CGCCTGTACT ATGGCAGCCG 1260  
 CTAGTCCCTG ACAACTTCCA CCCTGATTCC GGACCTGTA GATTGGGGGC CACCACCAGA 1320  
 TCCCCCTCCC AGGCTTCTCT CCCTCTCCCA TCAGCAGCCC TGTAACAAGT GCCTTGTGAG 1380  
 AAAAGCTGGA GAAGTGAGGG CAGCCAGGTT ATTCTCTGGA GGTGTGTGGA TGAAGGGGTA 1440  
 CCCCTAGGAG ATGTGAAGTG TGGGTTTGGT TAGGAAATG CTTACCATCC CCCACCCCCA 1500  
 ACCAAGTTCT TCCAGACTAA AGAATTAAGG TAACATCAAT ACCTAGGCTT GAGAAATAAC 1560

CCCATCCTTG TTGGGCAGCT CCCTGCTTTG TCCTGCATGA ACAGAGTTGA TGAAAGTGGG 1620  
 GTGTGGGCAA CAAGTGGCTT TCCTTGCCTA. CTTTAGTCAC CCAGCAGAGC CACTGGAGCT 1680  
 5 GGCTAGTCCA GCCCAGCCAT GGTGCATGAC TCTTCCATAA GGGATCCTCA CCGTTCCACT 1740  
 TTCATGCAAG AAGGCCCAGT TGCCACAGAT TATACAACCA TTACCCAAAC CACTCTGACA 1800  
 GTCTCCTCCA GTTCCAGCAA TGCTAGAGA CATGCTCCCT GCCCTCTCCA CAGTGCTGCT 1860  
 10 CCCCACACCT AGCCTTTGTT CTGGAACCC CAGAGAGGGC TGGGCTTGAC TCATCTCAGG 1920  
 GAATGTAGCC CCTGGGCCCT GGCTTAAGCC GACACTCCTG ACCTCTCTGT TCACCCCTGAG 1980  
 15 GGCTGTCTTG AAGCCCCGTA CCCACTCTGA GGCTCCTAGG AGGTACCATG CTTCCCCTC 2040  
 TGGGGCCTGC CCCTGCCTAG CAGTCTCCCA GGTCCCAACA GGCTGGGGAA GGTCTGCACA 2100  
 GACTGACCTG AGACCAGTA CAGGAAACCT GTAGCTCAAT CAGTCTCTCT WTAAGTGCAT 2160  
 20 AAGCAATAAG ATCTTAATAA AGTCTTCTAG GGTGTAGGT GGTTCCTACA ACCACAGCCA 2220  
 AAAAAAAAAA AAAAAAATC GAG 2243

25

(2) INFORMATION FOR SEQ ID NO: 145:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GCGAAGCTCT AATACGACTC ACTATAGGGA AAGCTGGTAC GGCTGCAGT ACCGGTTCCG 60  
 40 GGAATTCCCG GGTGGACCA CGCGTCCGCT TCGTGTGTC AAAATCCTCA CCTCCTTCAT 120  
 AACCATCTCC CACAATTAAT TCTTGACTAT ATAAATTTAT GGTITGATAA TATTATCAAT 180  
 45 TTGTAATCAA TTGAGATTTT TTTAGTCTT GCTTTTCTGT GACTCAACTG CCCAGACACC 240  
 TCATTTGACT TGAAACTGG AACANCTTGG GAATGCCATG GGGTTTGATA ATCTGCCAGG 300  
 GACATGAAGA GGCTCAGCTT CCTGGGACCA TGACTTTGGC TCAGCTGATC CTGNACATGG 360  
 50 GAGAACCAACC ACATTTTCTT TTGTGTGTC TTCTAGCAGC TGTTCGGGAG GACCKTGACC 420  
 CAAYAGTGTT CCCATGCTGT TTCTGTGAA ATGCTCTCGG CTATGTAGCA GCTTTTGATT 480  
 CCCTGCATAC CCTAGGCTGC TGCCCTATC CTGTCCCTTG TTTATAACAT TGAGAGGTTT 540  
 55 TCTAGGGCAC ATACTGAGTG AGAGCAGTGT TGAGAACTCG GGGAAATGG TGACTACTTT 600  
 TAGAGCAAGG CTGGGCATCA GCACCTGTCC AGCTCTACTT GTGTGATGTT TCAGGAAGTC 660  
 60 AGCCCTTTT TCTGCCTAGG ATAAGGAGCT GAAAGATTAA CTGGATCTY CTAATGGTCC 720



5 AAATCTTTTG GTCACATAA AGAGTCTCCA AATTAGAGAC TGCATGTTAG TTCTGGATGG 780  
 ATTTGGTGGC CTGACATGAT ACCCTGCCAG CTGTGAGGGG ACCCCGTTTT TAAGATGCAT 840  
 GGCCAAGCTC TCTGCAAATG GAAATGCTTA CACTGGGTGT TGGGGATGTT TGCTACCTCC 900  
 TGCTATTTTT GTGTTTTGG TTCTCCCACT ATGGTAGGAC CCCTGGCCAG CATGTGGCT 960  
 10 TGTCAATGCA GCCCCATGA CTACCTTCTC ATGCTCTGAG GTACTACTGC CTCTGCAGCA 1020  
 CAAATTCTA TTTCTGTCAA TAAAGGAGA TGAAAATPAA AAANAAAAA AAAAAACTCG 1080  
 NG 1082

20 (2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

30 CAAGCTGGTT TGAACTAGG GTCGGGCTC GCGCGTCGTG GTTGTTTGTC GCGCATCCC 60  
 CGCTTCGGG TTAGGCGGTT COTGCCCGCC CCCTCCTCTC CTCCCTTCGG ACCCATAGAT 120  
 CTCAGGCTCG GCTCCCCGCC CGCCGCAGCC CACTGTTGAC CCGGCCCCGT CTGCGGCCCC 180  
 35 GTGGCCACCA TGTCCCTGCA CGGCAACCG AAGGAGATCT ACAAGTATGA AGCGCCCTGG 240  
 ACAGTCTACG CGATGAAGTG GAGTGTGGG CCGGATAAGC GCTTTCGCTT GCGCCTGGCC 300  
 40 AGCTTCGTGG AGGAGTACAA CAACAAGGTT CAGCTTGTG GTTAGATGA GGAGAGTTCA 360  
 GAGTTTATTT GCAGAAACAC CTTTGACCAC CCATACCCCA CCACAAAGCT CATGTGGATC 420  
 CCGACACAA AAGGCGTCTA TCCAGACCTA CTGGCAACAA GCGGTGACTA TCTCCGTGTG 480  
 45 TGGAGGGTTG GTGAACAGA CACCAGGCTG GAGTGTTCG TAAACAATA TAAGAACTCT 540  
 GATTTCTGTG CTCCCTGAC CTCCTTGAC TGGAAAGAG TGGATCCTTA TCTTTTAGGT 600  
 50 ACCTCAAGCA TTGATACGAC ATGCACCTC TGGGGCTGG AGACAGGCA GGTGTTAGGG 660  
 CGAGTGAATC TCGTGTCTGG CCACGTGAAG ACCCAGCTGA TCGCCCATGA CAAAGAGGTC 720  
 TATGATATTG CATTTAGCCG GCGCGGGGT GGCAGGGACA GTTTGCCTC TGTGGGTGCT 780  
 55 GATGGCTCGG TCGGATGTT TGACCTCCGC CATCTAGAAC ACAGCACCAT CATTTACGAA 840  
 GACCCACAGC ATCACCCTCT GCTTGCCTC TGCTGGAACA AGCAGGACCC TAACTACCTG 900  
 GCCACCATGG CCATGGATGG AATGGAGGTG GTGATTCTAG ATGTCCGGGT TCCTGCACAC 960

	CTGTSGCCAG GTTAAACAAC CATCGAGCAT GTGTCAATGG CATGCTTGG CCCCCACATT	1020
	CATCCTGCCA CATCTGCACT GCAGCGGATG ACCACCAGGC TCTCATCTGG GACATCCAGC	1080
5	AAATGCCCG AGCCATPGAG GACCCCTATCC TGGCCTACAC AGCTGNAAGG WGAGATCAAC	1140
	AATGTGCAGT GGGCATCAAC TCAGCCCGAA YTGTCGCCAT CTGCTACAAC AACTGCCCTGG	1200
10	AGATACTCAG AGTGTAGTGT TGGTGGCGCT GTGCCCACGA GGCAGGGGCT TTTGTATTTC	1260
	CTGCCTCTGC CCCACCCCCA AAGTAAGAAG AAACATGTTT CCAGTGGCCA GTATGTCTTT	1320
	CATTGCTTTG CACCCACTGT TACCAGAAGC TGCTCTAGGA GTTCCTGGCC AGTCACCCCA	1380
15	TCGCCCTCTG TGGCAGACTC AGTGCTGTGT GCGCCTCCT CAGCCCAGGG CTGAGTTTAA	1440
	AGATTTTCTC TCCTTTCTC TTCTCTTTG GTTCCTCAAT TAAAAAATGT GTGTATATTT	1500
20	GTTTGTGAGG CGTTGTGTG AGGAGCAGTT CAGCCTCTGG CTGTGTCTAT TCCTCTGCCC	1560
	AGGTGTCTCT GTTTGCTGCC CAAGG/WKKT TTTTCATGCT CGTCCATGTC CATGTTCTGT	1620
	TTAGCACTWA CGTGGGAACA AATACCAATT TGTCTTTTCT CCTAGTATCA GTGTGTTTAA	1680
25	CAAAATTTAA CTTTGTATAT TTGTTATCTA TCAGGCTAAT TTTTATGA AAAGAATTTT	1740
	ACTCTCTGTC TTCATTCTT TGTCTTATAG TCCTCCCTCT TTGCACCTTC TTCTCTTCCC	1800
30	TCAGTGCTG GAGCTGGTAC TGGCCCCCTG GCCCCATGAG CAGTTTGCCT TCTTGAGTCA	1860
	CTGCCTGTGT AGTACATACC TGACCGGGAG TCCAAACCAC CTTGGTGCTC TGAAGTCCAC	1920
	TGACTCATCA CACCTTTCTT AGCCTGGCTC CTCTCAAGGG CATCTGGGC TTGTAAACAG	1980
35	ACATAGGAAG CCTCTGTTTA CCTGAAGCA CCAGTGTCCA GCCCATTGGT TCCCCTGCG	2040
	AGCATGGTAG AGCTGAGAGA AACAGGCTCT CAGGGTACCT GACTTGAGGG GAATCGTTTC	2100
40	ATGAAGCTGA ACTTCAAGCA TATTTCCAGT ACATTTCTTC AGAGTCTGTT TTTCCATCCA	2160
	AATATAAGCC CCAGGCCATT CCACTTAGTG TCTTTTCAAT GATAGGCAAG AATGATATCT	2220
	GACTTGAAC TCGGTGCTTC TGTGTTTGA GTTTACTGTG CCTGGTGGTA TATTTGGCAT	2280
45	TCTTTGGATT GAGTGTCTG AGGTGAGAGA GTCTTCCCGA GGCATCCTGT CTGTGCTTCC	2340
	AACCCTGAAC AAGACCTTAC ATGAGAGATG GACTGATGGA CTGCGGCAAT CCTGGGCTGT	2400
50	CAAGTGATA GATAGTTAAA AAGCATTATA CTGTGGGTAA TGAAAAGGA GGAAGAAAAA	2460
	AGAAGGAAAA GGAATTATAG ACCCCCAGGG TCAGCCAGTT AAGAGCTCTA CCCACACCTG	2520
	TCAACCCCTC TCTCCCCCAG TTTAGGTTCT GAGCAGTATT GGACTTGTAG CCTGCACTTG	2580
55	TCTTTGACT TGCAAGCCCG AGTGTCTTTC TGTATCTGA ATGAGTTCCA TGGAGGGGCA	2640
	TATGTGTGAT TCCACCGTTA GATGAGCCCT TGGGGCAGGC AGTTTGGGAT GTGCTCTTGG	2700
60	GGGAAAGTTG GCTGTTTCCT TGGCTCTGC TCCTACCCGA AGTTTATAAG TCCCTCTGAA	2760

	TTGCTCATCT GAGATTAGTA GAGTAGCAGG CCTGAAGGAT GATGGTTTTG TCCTCTTTGG	2820
	TTCTCACCTG CTTGAGAAGT AAAACAGTAA CTTTGTCTTT CTGGGCCCTT AAGCTTTTTT	2880
5	GGTTAAGTCT TCCTTTTCAG AAGTAGATGT CATTATATGC CAAAAGTCTA GCTCTTTGCT	2940
	TTACCATACA GGGACCTGTC CCAAAGAAAA AGGCTCTTTT TTTAGCCAGC ATATTTCCCC	3000
10	TTCTACCCCTT TTACTTTGTT GTTCTGATTT TAGGACTCTG GCTGGCCATG TGCTTGTGGT	3060
	TGCTCTCTCT GCATTTGCCA CTGGATTTGC ACTGCATCGT TTGGAGATAC AAAGCGAGCA	3120
	GTTCTTGGTC AGAACCCCTCC TCTGCTTTTC ATTGTGTTTG ATAATGCTTA CTGGGTCCTT	3180
15	CTCTCAAGGG TAGCAAGGCC AAGCTGATGG CTGCTTGTTC AGGAGGCCAT CAGTTCCCTC	3240
	CTGTGGAGAA GGGTCTGAAA TGGAACTCAG TGGTAGAAGG GGCTGGTCTG CTGGGCAGGG	3300
20	CTTACATCCA CTGAGTTCTA AGATTCCCTT CCGATCTGC ACCTACGCCCT GGTCTGTATG	3360
	GTGGAATTTG TCAGCTGGAA CTCAGAAACA ACAACTTGAA AAAAAAATAA TAATTAGAAC	3420
	ATATTTGCAT AAGATAGCTA TTTACTCTGG AAACCAACAA CTTTGTAGAT TTCCCTTGCC	3480
25	CTGTGGACGC CCAGCTCCTG TCATCCTTCC TTAGGTCCTG CAGTACAGTC TTCCCTGAA	3540
	TGCCACCGGG GACCCAGGGG GACTCCACCC CCTAAGCAA GCACACACAT ACTCAGATT	3600
30	GATGAGTTGC TGGTCTTTGA GTCCACGCTC TCTTACCCTC CTTTACTCC ACCAGCCCGA	3660
	CGACCCATGA CTGAGGAGGG GATTTCTACA GTCTCAGGAT TTAGAAAGTC TGTAAGCCAT	3720
	CCATGCTCCA GAAAGCACCG ATCTGTTGTA GTTGCAAAAA CAACTCTGTA ATTTGTTGAG	3780
35	GTTCTCAAAC TGACAGCCAG CGAGACTGGG TGGGAGGCCC TGGATCTGTT CTCCTGACT	3840
	GCGGGAGGAG CAGCCACTAG GACTTTAGCA GGAAGCCAC ATGGAGGCTC CGCCAGGCTG	3900
40	TGGCCAGCT GGTGATGGCC CTTTGTCTCC TGGCAGCCTG AGGCACAGCT GCCTGTATTG	3960
	TCCTCATCTG TTCTGACTGA AGGATGGAGG TGCTGAATAA ATTAGCCCTC AGGCTCTAC	4020
	CACCAGAGAG CTGGAGAATG GGTCCACGTC ATTCAGGAC CTGAATTTTT TATGCTCAGG	4080
45	AGCATTGGAA TCCTCTTCTT CCAGGGAGGA ATTAGCCTCC AAGGTTAGGA CTTGAAGAGG	4140
	GAAGGTATTT AATAACTGGG CGAGCATGGG TGTGGTGGCT CACACCTGTA ATCCAGCAT	4200
50	TTTGGGAGGC TGAGGTGGCC AGATCCCAAG GTCAGAAGAT CGAGACCATC CTGGCTAACA	4260
	TGGTGAAACC CCATCTCTAC TAAAAATACA AAATTAAATT GGCCGGGCGT GAA	4313

55

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1183 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5 GGCAGAGCCT CAAGCTGACT TGGATTATGT GGTCCCTCAA ATCTACCGAC ACATGCAGGA 60

GGAGTTCCGG GGGCGGTTAG AGAGGACCAA ATCTCAGGGT CCCCTGACTG TGGCTGCTTA 120

10 TCAKWWYGGG AGTGTCTACT CAGCTGCTAT GGTCAAGGC CTCACCCCTGT TGGCCTTCCC 180

ACTTCTGCTG TTGCATGCGG AGGCGATCAG CCTTGTGTTC CTGCTTCTGT TTCTGCAGAG 240

CTTCCTTCTC CTACATCTGC TTGCTGCTGG GATACCCCTC ACCACCCCTG GTCCTTTTAC 300

15 TGTGCCATGG CAGGCAGTCT CGGCTTGGGC CCTCATGGCC ACACAGACCT TCTACTCCAC 360

AGGCCACCAG CCTGTCTTTC CAGCCATCCA TTGCCATGCA GCCTTCGTGG GATTCCCAGA 420

20 GGGTCATGGC TCCTGTACTT GGTGCTCTGC TTTGCTAGTG GGAGCCAACA CCTTGCCTC 480

CCACCTCCTC TTTGCAGTAG GTTGCCCACT GCTCCTGCTC TGGCCTTTC TGTGTGAGAG 540

TCAAGGGCTG CGGAAGAGAC AGCAGCCCCC AGGGAATGAA GCTGATGCCA GAGTCAGACC 600

25 CGAGGAGGAA GAGGAGCCAC TGATGGAGAT GCGGCTCCGG GATGCGCCTC AGCACTTCTA 660

TGCAGCACTG CTGCAGCTGG GCCTCAAGTA CCTCTTTATC CTTGGTATTC AGATTCTGGC 720

30 CTGTGCCTTG GCAGCCTCCA TCCTTCGCAG GCATCTCATG GTCTGGAAG TGTTCGCCCC 780

TAAGTTCATA TTTGAGGCTG TGGGCTTCAT TGTGAGCAGC GTGGGACTTC TCCTGGGCAT 840

AGCTTTGGTG ATGAGAGTGG ATGGTGCTGT GAGCTCCTGG TTCAGGCAGC TATTCTGGC 900

35 CCAGCAGAGC TAGCCTAGTC TGTGATTACT GGCACCTTGGC TACAGAGAGT GCTGGAGAAC 960

AGTGTAGCCT GGCCTGTACA GGTACTGGAT GATCTGCAAG ACAGGCTCAG CCATACTCTT 1020

40 ACTATCATGC AGCCAGGGGC CGGTGACATC TANGACTTCA TTATTCWATR ATTGAGGACC 1080

ACAGTGGAGT ATGATCCCTA ACTCCTGATT TGGATGCATC TGAGGGACAA GGGGGKCGGT 1140

45 STCCGAAGTG GAATRAAATA GCGGGCGGTG GTGACTTGCA CCT 1183

(2) INFORMATION FOR SEQ ID NO: 148:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 734 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

60

GAATTGGGCA GAGTGAAGCA TTAGAATGAT TCCAACACTG CTCTTCTGCA CCATGAGACC 60

399

AACCCAGGGC AAGATCCCAT CCCATCAGAT CAGCCTACCT CCTCCTGGC TGCTGGCCAK 120  
 GATGTGCGCA GCATTACCTT CCACTGCCTT TCTCCCTGGG AAGCAGCACA GCTGAGACTG 180  
 5 GGCACCAGGC CACCTCTGTT GGGACCCACA GGAAGAGTG TGGCAGCAAC TGCTGGCTG 240  
 ACCTTTCTAT CTTCTCTAGG CTCAGGTACT GCTCCTCCAT GCCCATGGYT GGGCCGTGGG 300  
 GAGAAGAAGC TCTCATACGC CTTCCCACTC CCTCTGGTTT ATAGGACTTC ACTCCCTAGC 360  
 10 CAACAGGAGA GGAGGCCTCC TGGGGTTTCC CCRGGCCAGT AGGTCAAACG ACCTCATCAC 420  
 AGTCTTCCTT CCTCTTCAAG CGTTTCATGT TGAACACAGC TCTCTCCRCT CCCTTGTCAT 480  
 15 TTCTGAGGGT CACCACTGCC ARCCTCAGGC AACATAGAGA GCCTCCTGTT CTTTCTATGC 540  
 TTGGTCTGAC TGAGCCTAAA GTTGAGAAAA TGGGTGCCAA GGCCAGTGCC AGTGTCTTGG 600  
 GGGCCCTTTG GCTCTCCCTC ACTCTCTGAG GCTCCAGCTG GTCTGGGAC ATGCAGCCAG 660  
 20 GACTGTGAGT CTGGGCASGT CCAAGGCCTG CACCTTCAAG AAGTGAATA AATGTGGCCT 720  
 TTGCTTCTAT TTAA 734

(2) INFORMATION FOR SEQ ID NO: 149:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1405 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GGCACAGTGG ACCCCAGACT CCTCTCCGC CTTTCTCTGC CTGGGGAGAC CCACTGTGTG 60  
 40 CATGGCATCA CTGACTCCCA TACCTCTGGC TATCAAAGGT TTCTGCCATG GCCACCCTGG 120  
 AAGSAAACCA GAGGGAGGTA GACAGGGAGA TCAGGTCCCT TCTACTCTGG TTCTGTCTCT 180  
 45 GTGAAATTGT CTCAGGCTGG CTGTGTCCAG ARGGTCCCTG GTTCTCTCAE GGATGCCAAA 240  
 TCTACAAGAA TCTCTCCTCT TCCAGTTCCT ATAACCTCTC CTTCCCTTTG TCTCTTTAGA 300  
 CTTTGGAGTA GTAGCAGCCA GGTTCCTTCT ATCTCTGGGT TAGTGCATTA TCTCTGGTGG 360  
 50 CTCCCTTACC CAGGACTTTG GGAATGGTCT TTTTGTAAATA CATCTCCTC AAATAATTCA 420  
 ATTTTGAGTG TTCTGTATGT ATCCTGCTGG GAGGTTGTTA TATACAAATC ACTGTGCCCC 480  
 55 TTTAGCAGAG AAGGAGACTG AAGCTCAGGG AGGTAAAGTG TCTTCTCTA GGTGGTATG 540  
 TGGAGAAAGT GGCTGACTCG GCACTTGAAT GAGGTCCCTA GTTTCATGCT CGGAGGGCAA 600  
 AGANGAATGT CCAATGGCC TGAGATAAGC CTCTGGTAAA ATGTACTGTA CATAATAGGT 660  
 60 AATCAATAAA TGTGGCTGA TGACAAACAT GTTTCTTTG TTCATTAGTT ATAGTGATTA 720

TGTTCCTAAAT AACTCCMACA AGGAARTCAG CACATTTGGA ATATCAWTAT CTTTCCATGA 780  
 TAATATCTTT CCMYGGAAAG AWAATGATAT TCCMAACTGG GAGTGTCCCN ASCARATCTG 840  
 5 ANTCTGTGTA TTGGCCCTGG GGTGGGCCAG CCCCTTAGAC TCTATGGTCT CATTCCTTTT 900  
 GTTTACAAAA TTGAGATAAG GCCTTATTCT CTCGCCACCC CACCCATCCA TATTGTTTTG 960  
 10 AGAATAAAAT GAGAGGATGT GTGTCAAGGG TGTATTTTGG CAATAGTCTC TGAGCCATTT 1020  
 TCTGAGCACC TCCATACTGT TGACACTCAA GTAATATTTC ATCAGCATTC CATTCAGGNT 1080  
 CCTCCCTTAA TGAGGTGTCC GATGTACAAG AGTGTGAGG TGGCAAAGGA TGGGCTCCTG 1140  
 15 AGGAAACACT TAGGAAACTG GGCTTTCTGC CATTAAGA GACAAACCTT TGTGCTGACC 1200  
 TAATTAACT TTTTAAAT CAATTTGGAA AGTTAGCAAG CTAGCTCCTK TCCAGGWAAA 1260  
 20 ATAAGGAGTC AGTGCAATGAC CTAACCGGTC CCGGGCTGCT TGCCATTCCA AACAACGCA 1320  
 GTAAGTTTAT CACNTTCTTT CAGGACTGA GGTTCACAG CACGACTTG GATAGGAAG 1380  
 25 GATGTCCTAT GGGTCCACAT TGATG 1405

## (2) INFORMATION FOR SEQ ID NO: 150:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2890 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TTATATGCTA CAGCTACAGT AATTTCTTCT CCAAGCACAG AGGANTTTTC CCAGGATCAG 60  
 40 GGGGATCGCG CGTCACTTGA TGCTGCTGAC AGTGGTGGTG GGAGCTGGAC GTCATGCTCA 120  
 AGTGGCTCCC ATGATAATAT ACAGACGATC CAGCACCAGA GAAGCTGGGA GACTCTTCCA 130  
 45 TTCGGGCATA CTCACTTTGA TTATTCAGGG GATCCTGCAG GTTTATGGGC ATCAAGCAGC 240  
 CATATGGACC AAATTATGTT TTCTGATCAT AGCACAAAGT ATAACAGGCA AATCAAAGT 300  
 AGAGAGAGCC TTGAACAAGC CCAGTCCCGA GCAAGCTGGG CGTCTTCCAC AGGTACTGG 360  
 50 GGAGAAGACT CAGAAGGTGA CACAGGCACA ATAAAGCGGA GGGGTGGAAG GATGTTTCC 420  
 ATTGAAGCCG AAAGCAGTAG CCTAACGTCT GTGACTACGG AAGAAACCAA GCCTGTCCCC 480  
 55 ATGCCTGCCC ACATAGCTGT GGCATCAAGT ACTACAAAGG GGCTCATTCG ACGAAAGGAG 540  
 GGCAGGTATC GAGAGCCCCC GCCCACCCTT CCCGGCTACA TTGGAATTCC CATTAATGAC 600  
 60 TTTCCAGAAG GGCACCTCCA TCCAGCCAGG AAACCGCCGG ACTACACAGT GGCCCTTCAG 660

	AGATCGCCGA TGGTCGCCAG ATCCTCCGAC ACAGCTGGGC CTTCTCCGT ACAGCAGCCA	720
	CATGGGCATC CCACCAGCAG CAGGCCTGTG AACAAACCTC AGTGGCATAA AYCGAACGAG	780
5	TCTGACCCGC GCCTCGCCCC YTATCAGTCC CAAGGGTTTT CCACCGAGGA GGATGAAGAT	840
	GAACAAGTTT CTGCTGTTTG AGGCACAGAC TTTTCTGGAA GCAGAGCGAG CCACCTGAAA	900
10	GGAGAGCACA AGAAGACGTC CTGAGCATTG GAGCCTTGGA ACTCAGATTG TGAGGACGGT	960
	GGACCAGTTT GCCTCCTTCC CTGCCCTTAA AGCAGCATGG GGSTTCTTCT CCCCTTCTTC	1020
	CTTCCCTTT TGCATGTGAA ATACTGTGAA GAAATTGCC TGGCACTTTT CAGACTTTGT	1080
15	TGCTTGAAAT GCACAGTGCA GCAATCTTCG AGCTCCCACT GTTGCTGCCT GCCACATCAC	1140
	ACAGTATCAT TCCAAATCC AAGATCATCA CACAAAGATG ATTCACTCTG CCTGCACTTC	1200
20	TCAATGCCTG GAAGGATTTT TTTTAATCTT CTTTTTAGAT TTCAATCCAG TCCTAGCACT	1260
	TGATCTCATT GGGATAATGA GAAAAGCTAG CCATTGAACT ACTTGGGGCC TTAAACCCAC	1320
	CAAGGAAGAC AAACAAAAC AATGAAATCC TTTGAGTACA GTGCTTGTC ACTTGTTTAC	1380
25	AATGTCTCC TTTTAAAAA AAAAAAATGA GTTTAAAGAT TTTGTTTACA GAGTAAATAT	1440
	ATATCCATTT AATGATTACA GTATTATTTT AAACCTTAAG TAGGGTTGCC AGCCTGGTTT	1500
30	CTGAAAAACC AATATGCCG GACAGGGTGT GGCACACCA AGAAGACGGG AAGACCTGGC	1560
	TTGTGACCTT GGCTTCCCAT GTCCCTCTGG TCTCACCCTG GAAGTGCCCT ATCCTGGAAG	1620
	TATGAAATGT TAGCCAATTA ATACCAAGAC ACCTCATCTG CTCCTTCCCC AGTGSATGGG	1680
35	GTCTTCTGT AAAACTGTTT GCACATGGCC AGGGGAGGGA ACTAGGACCC TTGTGTCTGT	1740
	TCTGAGCCTT ATGGAGGCAG GACGGTGTCA TTGGCGGATG TGTCTCTCTC CATTGAGATG	1800
40	GATGGCAAAC CCCATTTTTA AGTTATATTT CTTTGATTTT TGTTAATTTA GAGGTGTAGG	1860
	TTTTGTTTTT TGTTTTTTTG TTTTTTTTAA AGAGAAACAT TTATAACTGG ATAGCATTGC	1920
	AGTGAAAGCA GCTTGGGATG TTGGAGCTAA TGCCAGCTGT TTATACTGCT CTTTCAAGAC	1980
45	AGCCTCCCTT TATGGAATG GCATTAGGGA ATAAACAAGC CTTTAAACGT GATAAAAGAT	2040
	CAAAAACCTG GTTAGACATG CCAGCCTTTG CAAGGCAGGT TAGTCACCAA AGACTAACCT	2100
50	CCAAGTGGCT TTATGGACCC TGCATATAGA GAAGGCCTAA GTGTAGCAAC CATCTGCTCA	2160
	CAGCTGCTAT TAACCCTATA ATGACTGAAA TGACCCCTCC ACTCTATTTT TGTGTGTGTT	2220
	TGCACAGACT CCGGAAAAGT GAAGGCTGCC AATCTGAGTA GTACTCAAAT GTGAGGAAC	2280
55	GCTGGTCTTG GATTTTTTTT CCATTAAATT CAGCTGATCA TATTGATCAG TAGATAAAGC	2340
	TAAATAGCTT CAAATTTTAA AAGTGGAATT GCAGTGTGTTT TTCACTGTAT CAAACATGT	2400
60	CAGTGCTTTA TTTAATAATT CTCTTCTGTA TCATGGCAAT TGTCTACTTG CTTATTACAT	2460

TGTCAATTAT GCATTTGTAA TTTTACATGT AATATGCATT ATTTGCCAGT TTTATTATAT 2520  
 AGGCTATGGA CCTCATGTGC ATATAGAAAG ACAGAAATCT AGCTCTACCA CAAGTTGCAC 2580  
 5 AAATGTTATC TAAGCATTAA GTAATTGTAG AACATAGGAC TGCTAATCTC AGTTCCGCTCT 2640  
 GTGATGTCAA GTGCAGAATG TACAATTAAAC TGGTGATTTC CTCATACTTT TGATACTACT 2700  
 10 TGTACCTGTA TGTCTTTTAG AAAGACATTG GTGGAGTCTG TATCCCTTTT GTATTTTAA 2760  
 TACAATAATT GTACATATTG GTTATATTTT TGTGAAGAT GGTAGAAATG TACTATGTTT 2820  
 ATGCTTCTAC ATCCAGTTTG TACAAGCTGG AAAATAAATA AATATAACAT AAAAAAAAAA 2880  
 15 AAAAAAAAAA 2890

20 (2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2399 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

30 GAACCTTTTCC ATCTGGCAA CCGAAACTC CATCCCCATT AAACCAACTC CCCCTTTTGG 60  
 TTTCCCCCCC AGNGGAATAG AATTGGACN CCCATATAAA TCCAGGAAAC CACCTAAATT 120  
 CTTTAGTNGT TTGTGTTTGC AAGATCTAAG GTCATGGTAA ACATTAAGTT CTTAAAATTT 130  
 35 TTGGGAGGGA CCAGTGCACC TCTCCCTCTG AATTGTTTNC CATTTTAAAA TTGGAGTAAG 240  
 GTTTTAAAT GTCTNATTCC ATTGGAAGGG TMTGTTATTT CATTTTGACC CCAGAGGGGA 300  
 40 GAGGCACATT TTAATATCA GAATTAGATT AGCTTTGAGT TTGTACAATT GGGAACATAA 360  
 TAGATTTTCA TAAATTATGT GTGCCTTGTT GGAAGTGTCA ACTGTCTTTA TGTCTGCTTG 420  
 TAAAAGTTTC AAAATATGTT TTCCCTCAA AAGGCAACGT TACTTCATTT GCTTGAATAT 480  
 45 TATGATAGGA ATGCTTACTG ATATTACTTG ATAGTCATAT ATAGCCTAGG AAATTTAACA 540  
 TATATATAAC TATAGCAGTA TTAATAATGA TAGTTGTACT TCTTTAAAAC ATTAAATTTG 600  
 50 AGGAAACTTT AATGCTGTCT CGTGTACATT GCTTTACTAC AGTGAGGGGG AATATCCTTT 660  
 AGATTGAGCC TCAATTTACT CGTTAGTAGT ATGTGAACTC TGGTATAAAA ACGTAAACTA 720  
 GACAGTAGAG CCGATGAATT AAAATTGTAA ATTGCTACAT TGGCATTTTC TACCTCCTTT 780  
 55 TCTGTCAGAG TATTACTTTT TCCAGCATTT ATTCTTATTT GTGAGTAAAG ACGAAATGGG 840  
 AACCTGAGGT TAAAATTGAC ATTTTGTGTT CATTGAGAAT TTAAGCAGTA GGTACAGGAG 900  
 60 AAGTGACTTG TCACATTAAT TTGGTGCTA AATCTGTAAC TACAAGTTGT GATCGACATG 960



	TACAAAATGT CTAAGAAAGG TCATATGCTG AATATTTTAC TTTTCCTGTA TAGTCTGCAT	1020
5	GATTTGTTTC ATAAACCCAG CTTATTTTCCT CCAAAAAGCA AAATGGTCCT GTAATTTTTC	1080
	AAGTAAATA AACGTGCCAT TTTGTCTGCA ATCTATAATT TCAGGAAGTT ATTGRAAGTT	1140
	CTGACTCAGG GCTTTTTAAC AGTTCAAGCA ATTGTCAGTT ATATTTTGGA AACTCCATCT	1200
10	GTGTAATTCT CCAGTGCCCTT GAAAGAATTA TTAAGTTGGC AACACTATTA AACTTTTATA	1260
	AAGATGGTC TTTAGTGCAC GTGTATCATT ATATACACGT TTTAAAGTCA TATGCTTAG	1320
15	CTTGTAATA ATGATTCTGC ATGTGTGCTG GGTITGGGTA ATTCTTTAAA GGAAGTTTTC	1380
	TAGATTTGCA CTGTATGTTT GTTTTTTAAA AACTGATTAT TTATGGCCGT GACTCTGTTA	1440
	CCAGAAAAGT AATCTAATT AAGTTATTAT GCAAAGTCAT CTATAAGTAG CATCTGGGAA	1500
20	GAGGAGATSG AGGCCACAGT TTGCTATTTT AGTATGAAAG GAGGATCTGT TTGGGAAACA	1560
	TAGATTGTCT TCCCTCATA TGAGGGGAAA AAAAAAGACC CTTTGTTCAT ATGGATTCTG	1620
25	TTGTAAAAA TTATTTTTAA AGGAAATCAC AAATTGTATG TCATTCTTAA TGCTAGTCTT	1680
	ATAGAATAAA TCCATAAAAT TGTTTTTATG TTCAGTATGT TTATGTCATT CTAAATGCAG	1740
	CAAAITCAAT GATAGCAGTT CAATTGACTC ATAGCAGTGT TTTGTATTTT TTCTAATTCT	1800
30	TTAGCTTTCA ATATGGATT AAAGTCTTGT TTGTGAATAT AGTTTCCGTA TGGCAAATGA	1860
	TTTCTTGCTT ATTAGCTTTT GTTAAAGAAAT GCTTAGTAAG AGCTAAGCTT TTTAAAGTAA	1920
35	TGCAAAACAT TATCGTTAAT AAAACCTATG GTGTAATATC ATATAATGCT TTTCTTTGAT	1980
	CTTTGGAGAA TTATCTTTT ATAGTAGTAT ACATGAATTT TGATTTTTTA AGCATTTAAA	2040
	AACAAATCTC AATACATTAA AAAACCTGTT ATTGTAAAA RGGAAATTAC CATGCCCTTA	2100
40	AGAAACAAGG ATGTACATCT TCAATTCAGC ATAGTGTCC ACATCTAGAA GGCTCTCATT	2160
	GCAGTTGTTT ACAGTTAAGG TACCTCTATC TAAAGGGCCA AAGAAGCATT TCATATTTTA	2220
45	ACACCTCACA TTCTTTTCAGG ATTAAGACAT ATGAAAATAG TCTGAATAGG ATAAATTTGG	2280
	ATAGGAAGTA ACTTAACCAG TCTGGGAAGA TTCAGGCTTT TTCTATKAAA AAGCTTATTC	2340
50	CTCTTCACAA CTCNGGTGGT AGGNTTTCAT TTTTCAAGAG GGTAGATATT TTTAAAGCCA	2399

## (2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

CGTGCCTGTA GTAAGCTCAT CCTGCTTTT GAGATGGTGA TGGGTGCCAA GGACAATGTT 60  
 5 TACCACCTGG ACTGCTTTGC ATGTCAGCTT TGTAAATCAGA GATTNTGTGT TGGAGACAAA 120  
 TTTTCTCTAA AGAATAACWT GAYCCTTTGC CARACGGACT ACGAGGAAGG TTTAATGAAA 130  
 GAAGGTTATG CACCCCMGGT TCGCTGATCT ATCAACATCA CCCCATTAAAG AATACAAAGC 240  
 10 ACTACATTCT TTTATCTTTT TTGCTCCACA TGTACATAAG AATTGACACA GGAACCTACT 300  
 GAATAGCGTA GATATAGGAA GGCAGGATGG TTATATGGAA TAAAAGGCGG ACTGCATCTG 360  
 15 TATGTAGTGA AATTGCCCCA GTTCAGAGTT GAATGTTTAT TATTAAAGAA AAAAGTAATG 420  
 TACATATGGC TGGATTTTTT TGCTTGCTAT TCGTTTTTGT GTCAGTTGGC ATGAGATGTT 480  
 TATTTTGGAC TATTGTATAT AATGTATTGT AATATTTGAA GCACAAATGT AATACAGTTT 540  
 20 TATGTGTTA CCAATTTGTGT TCCATTGCT YCTTTGTATT GTTGCAITTA GTACAATCAG 600  
 TGTTTAACT TACTGTATAT TTATGCTTTC TGTATTTACC AGCTATTTTA AATGAGCTGT 660  
 25 AACTTTCTAG TAAAGAATTG AAAAGCAAAT COTCACTAAA GGATACACAG GATAGGATAA 720  
 AGCCAAGTCN CATCAACATT AAAAAATACT AAAANANAAA ACACAAAAAA AAAAAANCCC 780  
 GGGGGGGGCC CGGAACCCAT TC 802  
 30

## (2) INFORMATION FOR SEQ ID NO: 153:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: -461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

CTAGGAGCAC CGAGCAGCTT GGCTAAAAGT AAGGGTGTGG TGCTGATGGC CCTGTGCGCA 60  
 45 CTGACCCGGG CTCTGCNCTC TCTGAACCTG GCGCCCCCGA CCGTGGCCGC CCCTGCCCCG 120  
 AGTCTGTTCC CCGCCGCCCA GATGATGAAC AATGGCCTCC TCCAACAGCC CTCTGCCTTG 180  
 50 ATGTTGCTCC CCGCCGGCCC AGTTCTTACT TCTGTGGCCC TTAATGCCAA CTTTGTGTCC 240  
 TGAAGACTC GTACCAAGTA CACCATTACA CCACTGAAGA TGAGGAAGTC TGGGGGCCGA 300  
 GACCACACAG GTGGGAACAA GGACAGGGGG ATTAAAGCAG TCAAAAGGAA AAACATGTTA 360  
 55 AGACCTTAGA CTTGTATATT GACACACTTG TACCTTGTA GGCAGAGGAA TGTAATTAAA 420  
 AAGCACTTAT TTGGCWNRAA AAAAAAAAAA AAAAAAAAAA C 461

60

## (2) INFORMATION FOR SEQ ID NO: 154:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2388 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

5 GGGCAGCGGT CCGAAAGCGG AGAAGCGCTGG TGGGCGCTGTT GTGGAGTACG CTTTGGACTG 60  
15 AGAAGCATCG AGGCTATAGG ACCGAGCTGT TGCCATGACG GGGCAGGGGG GCTGGTGGCT 120  
AACCAGCGCC GCGGCTTCAA GTGGGCGATT GAGCTAAGCG GGCTGGAGG AGGCAGCAGG 180  
20 GGTGGAAGTG ACCGGGGCAG TGGCCAGGGA GACTCGCTCT ACCCAGTCGG TTACTTGGAC 240  
AAGCAAGTGC CTGATACCAG CGTGCAAGAG ACAGACCGGA TCCTGGTGGG GAACCGCTGC 300  
TGGGACATCG CTTTGGGTCC CTTCAAACAG ATTCCCATGA ATCTCTTCAT CATGTACATG 360  
25 GCAGGCAATA CTATCTCCAT CTTCCCTACT ATGATGGTGT GTATGATGGC CTGGCGACCC 420  
ATTCAGGCAC TTATGGCCAT TTCAGCCACT TTCAAGATGT TAGAAAGTTC AAGCCAGAAG 480  
30 TTTCTTCAGG GTTTGGTCTA TCTCATGGG AACCTGATGG GTTTGGCATT GGCTGTTTAC 540  
AAGTGCCAGT CCATGGGACT GTTACCTACA CATGCATCGG ATTGGTTAGC CTTCAATTGAG 600  
CCCCCTGAGA GAATGGAGTT CAGTGGTGGG GGAAGTCTTT TGTGAACATG AGAAAGCAGC 660  
35 GGCTGGTCCC TATGTATTTG GGTCTTATTT ACATCCTTCT TTAAGCCCAG TGGCTCCTCA 720  
GCATACTCTT AAACATAACA CTTATGTATA AAAGAACCAA AAGACTCTTT TCTCCATGGT 780  
40 GGGGTGACAG GTCTAGAAG GACAATGTGC ATATTACGAC AAACACAAAG AAACATATACC 840  
ATAACCCCAAG GCTGAAAATA ATGTAGAAAA CTTTATTTTT GTTTCCAGTA CAGAGCAAAA 900  
CAACAACAAA AAAACATAAC TATGTAAACA AGAGAATAAC TGCTGCTAAA TCAAGAACTG 960  
45 TTGCAGCATC TCCTTTCAAT AAATTAAATG GTTGAGAACA ATGCATAAAA AAAGTTGCAC 1020  
AAGTTCCTTA TTTTCCTTAA TATTTCACTT CTATTTAATA CAAGCTGGGA CATAAAAATT 1080  
50 CTGTTGGGGA TACCTGGGGG AAGATGTGAG AAACATATGC TGAATTCAGC TTATACATGA 1140  
TGAAAAGAAA AACCAGACAA AAGGAGCACA TAAATATGCA TACAGTGTA CTTGTTATTAT 1200  
TTTAATACCC ACGATAAGGG ATTTTGTGTA GCATGTTTAG GGGGAACGAG GATTGGTGGG 1260  
55 ATCCTTGGGG CCACAGGAAT CTGAGGCAAC GGAAGATATA TAGAGTGATC GTCCCCCTGC 1320  
CGAAGGAACC TGGCAYCTGT CAAGCAGATG CTGCAGTTCA AACTTCAGCT TTTAAGATAG 1380  
60 ATAGCTATTS AAGGCAGAGG GTCAGCAGGA GATGTGTAT TTCTAATCTA CCCTGGTAAA 1440

5 GTCATAGGTA AGACTCAAAA GCGGGATCTT ATTCAAAAGG CAGGTATTTT CTTTGTTTTC 1500  
 TGTCTTGAAG TAGCCCCCTC CCTAAGGTG CATTCTCTCA AGTTTTCAGT ATTGCTTTAT 1560  
 10 TTGCAGTGAT TAAAAGAGAT GAGAGACTTT GGAGACAGAC AACGTAAGCA ACACATACAC 1620  
 ACATGAAATA CTCTAGACAG AGATGAATAT AAATCTGGCC TAATAACCAG TTTTCCATGT 1680  
 AACAGTGATT TTGTGTTTCG GGTGAAGCA GTGGTTATAT TAAAAGCCAC TAATTCCTTT 1740  
 ATCCCTTTAA AAGATTTTTA CAATTCTCCA ACCACAAACA GCACTTCTAA AACTAATTTT 1800  
 ACTTTCTGCC CATAATTTGT TCTACATGGA AAAAAAAT ATTACTTTGG CCAGGGGTGT 1860  
 15 GTGTAAATGT GGCAGAATTC CTAGGCAGGC TGACCTTTAC AGTATGGGCC TTTAAGATAC 1920  
 TGGATCCTGG TTGGGCAACA AGTGTACGC CTGAAGTTTC TGAAAACAAA TTAGAAGACT 1980  
 GTTGGCTTGG CTAATCTCGT AGTTCAGGCC CAAGTTTCTG TAGTCAGAT GAAGAATAAA 2040  
 20 ATTGAAAGAA AAAGGGGGAA ATGCTTATAC TTGGCATTAA GTTGAATGCC TCAAGTCTTA 2100  
 ACTATGGCTT TGTAGATGAG GCAAAAGATT TCTTAGTGGT AAAATTTCTT CACAGGTCA 2160  
 25 ATGCCAATCT GTATGCCATT TTAGTAAAGT AGGTAAGGAG AGTAGCCGCT CAGTAACTTT 2220  
 GGGACTAAG AAAGAGTGTG GCTCTAGAAC TTCCAATCCC ATTGCTAGAT GTGCCCTTTA 2280  
 AAAGATGGTC CAGTGCTTTC AGGGAAGGAT GTTTAGCCAG TTTTCCTAGT ATTTGTTCTT 2340  
 30 TAAGATTTTT TGACCTGTGC TTAATAAGAC GGACCGGTGG GTCGACCC 2388

35

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 642 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

45

AAAACAGACC ATTTAAAAAC TCAGACAAGA TTATATTTAA TATATTAATT ACTAAAAAGG 60  
 CACAAGATTA CACTGAACAT ATTAGCTACT AAAAAGGCAC TGCTAAGACA TTCAAGCAAA 120  
 50 TAGCTATTAC ACACTACTGC AGATTTTACA GGTTCCTAAT TCTAAGATAT GTTTGAAAAA 180  
 TCCGTGAGTA TTCCAAAATA TATTTAATAA TGGAATATCT GCATTAATAT ACCATCCATG 240  
 TGTFTTACCC ATTTGCCCTA ATATTGAATA TACTGTTTAC CTCACACTAA AAAGAAAACC 300  
 55 AGAAGCCTTA TTTGTGATTT TGGGACTGGA AGCTTCCATT TTTGTGTCAA AATGAATCC 360  
 TGATTCTTAT GGAAATCTCT GTTATTAAGA TATTTCAAGA TGAGACAACA CTGAAGATCA 420  
 60 AATTGTGTTT AGTATCACTA TCTTCTCTCC TGGTTTCTCT CTTACTCCTC ATCCTCCGAG 480

AATCTACCAG TTTATGCTAG AAAGATGGGA ACCTTATTTG AATGTGTTTT TTTTTTTCCA 540  
TGATGTCCAA TTTTGTGTG GGAAGGATT TGGATAAAAT TTTGTTTAA ATTTTGCTAG 600  
ATTTTATCT ATACAAATTT AAATAAAAT ATGTTTTGTA AG 642

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

GCCGCTGCCC CTCCACGGAG TTGCTGATCA TCTGGCTGT GATCCACAAA CCGGTTCTT 60  
TGTCCTCTCT AATATCAAA AGTGGATTGC CTTGCTGCAG AGGGGAACT GCACGTTTAA 120  
AGAGAAAATA TCACGGGCGG CTTTCCACAA TGCAGTTGCT GTAGTCATCT ACAATAATAA 180  
ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GAGCATATTA TTGCTGTCAT 240  
GATAACAGAA TTGAGGGGTA AGGATATTTT GAGTTATCTG GAGAAAAACA TCTCTGTACA 300  
AATGACAATA GCTGTGGAA CTCGAATGCC ACCGAAGAAC TTCAGCCGTG GCTCTCTAGT 360  
CTTCGTGTCA ATATCCTTTA TTGTTTGTAT GATTATTTCT TCAGCATGGC TCATATTCTA 420  
CTTCATTGAG AAGATCAGGT ACACAAATGC ACGCGACAGG AACCAGCGTC GTCTCGGAGA 480  
TGCAGCCCAAG AAAGCCATCA CTAATGTGAC AACCAGGACA GTAAAGAAGG GTGACAAGCA 540  
AACTGACCCA GACTTTGATC ATTGTGCACT CTGCATAGAG AGCTATAACC AGAATGATGT 600  
CGTCCGAATT CTCCCTGCA AGCATGTTTT CCACAAATCC TGGGTGGATC CTTGGCTTAG 660  
TGAACATTGT ACCTGTCTTA TGTGCAAACT TAATATATTG AAGGCCCTGG GAATTGTGCC 720  
GAATTTGCCA TGTACTGATA ACGTAGCATT CGATATGGAA AGGCTCACCA GAACCCAAGC 780  
TGTTAACCGA AGATCAGCCC TCGGCGACCT CGCCGCGGAC AACTCCCTTG GCCTTGAGCC 840  
ACTTCGAACT TCGGGGATCT CACCTCTTCC TCAGGATGGG GAGCTCACTC CGAGAACAGG 900  
AGAARTCAAC ATGTCAGTAA CAAAGAATG GTTTATTATT GCCAGTTTGT GCCTCCTCAG 960  
TGCCCTCACA CTCTGTACA TGATCATCAG AGCCACAGCT AGCTTGAATG CTAATGAGGT 1020  
AGAATGGTTT TGAAGAAGAA AAAACCTGCT TTCTGACTGA TTTTGCCTTG AAGCAAAAAA 1080  
GAACCTATTT TTGTGCATCA TTTACCAATC ATGCCACACA AGCATTATT TTTAGTACAT 1140  
TTTATTTTTT CATAAAATTG CTAAAGCCAA AGCTTGTAT TAAAGAAAT AAATAATAAA 1200

ATAAAAAAAAA AAAAACCCCG GGGGGGGCCC GGTCCCAAT TGGCCCTATG G

1251

5

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 2127 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

20

CCGGCGGGAG AGGAAGCTG CAGCGAGAGG CGCGGATCTC AGCGCGGGAG CAGTGCTTCT 60

GCGGCAGGGC CCTGAGGGAG GGAGCTGTCA GCCACGGAAA ACCGAGAACA CCATCACCAT 120

GACRACCACT CACCAGCCTC AGGACAGATA CAAAGCTGTC TGGCTTATCT TCTTCATGCT 180

GGGTCTGGGA ACGCTGCTCC CGTGGAAATT TTTTCATGACG GCCACTCAGT ATTTCAAAA 240

25

CCGCCTGGAC ATGTCCGAGA ATGTGTCCTT GGTCACTGCT GAACTGAGCA AGGACGCCCA 300

GGCGTCAGCG CACCTTGCCG TGAGCGGAAC TCTCTCAGTG CCATCTTCAA 360

CAATGTGATG ACCCTATGTG CCATGCTGCC CCTGCTGTTA TTCACCTACC TCAACTCCTT 420

30

CCTGCATCAG AGGATCCCCC AGTCCGTACG GATCCTGGGC AGCCTGGTGG CCATCCTGCT 480

GGTGTCTCTG ATCACTGCCA TCCTGGTGAA GGTGCAGCTG GATGCTCTGC CCTTCTTTGT 540

35

CATCACCATG ATCAAGATCG TGCTCATTAA TTCATTTGGT GCCATCCTGC AGGCGAGCCT 600

GTTTGGTCTG GCTGGCCTTC TGCCTGCCAG CTRACACGGC CCCCATCATG AGTGGCCAGG 660

GCCTAGCAGG CTTCTTTGCC TCCGTGGCCA TGATCTGCGC TATTGCCAGT GGCTCGGAGC 720

40

TATCAGAAAG TGCCTTCGGC TACTTTATCA CAGCCTGTGC TGATKATCATT TTGACCATCA 780

TCTGTTACCT GGGCCTGCCC CGCCTGGAAT TCTACCGCTA CTACCAGCAG CTCAAGCTTG 840

45

AAGGACCCGG GGAGCAGGAG ACCAAGTTGG ACCTCATTAG CAAAGGAGAG GAGCCAAGAG 900

CAGGCAAGA GGAATCTGGA GTTTCAGTCT CCAACTCTCA GCCACCAAT GAAAGCCACT 960

CTATCAAAGC CATCTGAAA AATATCTCAG TCCTGGCTTT CTCTGTCTGC TTCATCTTCA 1020

50

CTATCACCAT TGGGATGTTT CCAGCCGTGA CTGTTGAGGT CAAGTCCAGC ATCGCAGGCA 1080

GCAGCACCTG GGAACGTTAC TTCATTCCTG TGTCTGTTT CTTGACTTTC AATATCTTTG 1140

55

ACTGGTTGGG CCGGAGCCTC ACAGCTGTAT TCATGTGGCC TGGGAAGGAC AGCCGCTGGC 1200

TGCCAAGCTG GNTGCTGGCC CGGCTGGTGT TTGTGCCACT GCTGCTGCTG TGCAACATTA 1260

AGCCCCGGCG CTACCTGACT GTGGTCTTCG AGCAGCATGC CTGGTTCATC TTCTTCATGG 1320

60

CTGCCTTTGC CTTCTCCAAC GGCTACCTCG CCAGCCTCTG CATGTGCTTC GGGCCCAAGA 1380

AAGTGAAGCC AGCTGAGGCA GAGACCGCAG AGCCATCATG GCCTTCTTCC TGTGTCTGGG 1440  
 TCTGGCACTG GGGGCTGTTT TCTCCTTCCT GTTCCGGGCA ATTGTGTGAC AAAGGATGGA 1500  
 5 CAGAAGGACT GCCTGCCTCC CTCCTGTCTT GCCTCCTGCC CTTTCTTCTT GCCAGGGGTG 1560  
 ATCCTGAGTG GTCTGGCGGT TTTTCTTCTT AACTGACTTC TGCTTTCCAC GCGTGTGCT 1620  
 10 GGGCCCGGAT CTCCAGGCCC TGGGGAGGGA GCCTCTGGAC GGACAGTGGG GACATTGTGG 1680  
 GTTTGGGGCT CAGAGTCGAG GGACGGGGTG TAGCCTCGGC ATTTGCTTGA GTTTCTCCAC 1740  
 TCTTGGCTCT GACTGATCCC TGCTTGTGCA GGCCAGTGGG GCTCTTGGG CTTGGAGAAC 1800  
 15 ACGTGTGTCT CTGTGTATGT GTCTGTGTGT CTGCGTCCGT GTCTGTCAGA CTGTCTGCCT 1860  
 GTCTGGGGT GGCTAGGAGC TGGGTCTGAC CGTGTATGG TTTGACCTGA TATACTCCAT 1920  
 20 TCTCCCTGCG GCCTCCTCCT CTGTGTCTTC TCCATGTCCC CCTCCCAACT CCCCATGCCC 1980  
 AGTTCCTACC CATCATGCAC CCGTACAGT TGCCACGTTA CTGCCTTTTT TAAAAATATA 2040  
 TTTGACAGAA ACCAGGTGCC TTCAGAGGCT CTCTGATTTA AATAAACCTT TCTTGTTTTT 2100  
 25 TTCTCCATGG AAAAAAAAAA AAAAAA 2127

30

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1625 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

40 CAAAAGATCT ATAATCAGCA CATTGTTTAT GTAAGTTGGA CAANAAAAAT TCTTCCCTTT 60  
 TATGTCCACC CTTCCTATGA TTGCAAGACA AAATTTCCCT CTTTACCTC ATCCCTATAA 120  
 45 CATGGGAGGC TGAGAAAAAT GAGGGGAGAT GGAACCAGAT ACAAGGAGAT CCAATAAGAG 130  
 AAGCTTATTT AAATATTGTG AAATAAAGGA AGAMCCAAAG CATTTTTTTA AGTGGGGAAT 240  
 50 CCTTTTGAAC AGTTATTATT TATCCATATT ATTAAYAACA TCTTTTCTGA CAAATCCAT 300  
 CAGATGAAGT GTAATGGAT AATCTTTTAA TGCATCTAAA CCTAGAAAGT TTCACTTACT 360  
 GTTCATGTCC GGTTCACAGA ATGTGAAAT GGTGTGTGGT TTTGCTTCC AAGTTCTTCT 420  
 55 CTGCTCCTC TTAATTCTCT AATTCATGT CTTACAGAAG AATGAGAAAT TTCTTTCTTA 480  
 CTTGAGTATC ATGCTCTAAA AACTTGGCT TCAGTCACAG AAACGCTGGC TCTCCTGTGC 540  
 TTATATTGAA GCGAAGTCCC TTAAATTCTT GGGCCCTCTT ATATTTTAA GGTGCAAAAT 600

60

	TTGAAGTCTC AGTCACCAGA CACAGGTTCT ATACAATTAA TGATGAGCTG GAGAAGTAAT	660
	ATGTAGCTAA TTTTTCRAAA GCATTGAATA TACTTTCCGG AAAGAAAACA GAAATTBAAT	720
5	ATTGCCACAT CTTGCCAGAA TCCCATCTGA CACCTTAECT TTGTGAGGTT TCCTACAAC	780
	TGCTAATCAA GTTTTATACA TTCTAAATCT CCCCAGTTTC TTTGGGGCTG GAAGATGCAA	840
10	CTTCCATTTA ATAGAACTT TGAAATCTTG GGGTAAGGGA GCAGTGGGGG GACTAGGGAG	900
	AAGGATAAGA AATAGAATTA TTGAAAAGCC CCCACCAGGG ACCTTCCTGG CCAGAATATG	960
	CAGAGTAATT CCTGCTGGCT TCACCTTTGA AAGTCCTCG AAACATATGCA GATGAACTG	1020
15	AGTCTGTTTT TGATATTGTC AGATGTATTC TACCTTGGAA GTCCCNACAC CTAAACTGGA	1080
	ATTCTTGTAT TTACATCTCC TCCACTGTCC CCCACACCAC CCCTCAATTC CTGCTGCCCC	1140
20	TGCTAATGTT AAGCATTTTT CTCTTGTAT CATCAGGTTT ACATTAAAAM CAGTACTTA	1200
	CAAACTGACT TGAAGCACAG ATACTTTTAC GAATGTGATA AAATATTTTC TTAAGAAAAG	1260
	GAAAGAGGAT GTGGGTCAA TAAACACCG CATGGATGTT GATTGGTGAA TACTGGTGTA	1320
25	AGAAAAGGGA GCTCAGGAAT TTTTATTACT GTATTGTAA ATGAGTTTGA AGGAATTGT	1380
	AAATGCCACT GGTACATTTT TAAGGTGACA CATTTGCTCC TTATAAAGTT ATTAAAAATT	1440
30	ACAGGGTAAG CTTAAATGAC GTTTGCCAGT AGTTTTACTT TATATAATCA ATATTGATAT	1500
	TGTTGCTGAA CTATGTAECT TTATGATGCA TTTTTCAGTC CCTTTTCAGA GCAAATGCTT	1560
	TTGCAATGGT AGTAATGTTT AGTTTAAATT GACTTAATAA ATTTMTACCT GAGCAAAAAA	1620
35	AAAAA	1625

40 (2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1627 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

50	CGGGGTCACC AGTTATTAGA GGAAGTAACA CAAGGGGATA TGAGTGCAGC AGACACATTT	60
	CTGTCCGATC TGCCAAGGGA TGATATCTAT GTGTCAGATG TTGAGGACGA CCGTGATGAC	120
55	ACATCTCTGG ATAGTGACCT GGATCCAGAG GAGCTGGCAG GAGTCAGGGG ACATCAGGGT	180
	CTAAGGGACC AAAAGCCTAT GCGACTTACT GAAGTCCAG ATGATAAAGA GCAGGAGGAG	240
	GAGGAGAATC CACTGCTGGT ACCACTGGAG GAAAAGGCAG TACTGCAGGA AGAACAGCC	300
60	AACCTGTGGT TCTCAAAGGG CAGCTTTGCT GGGNATCGAG GACGATGCCG ATGAAGGCCC	360



	TGGAGATCAG TCAGGCCAG CTGTTATTG AGAACCGG/G GAAGGGACGG CAGCAGCAGC	420
5	AGAAGCAGCA GCTGCCACAG ACACCCCTT CCTGTTTGAA GACTGAGATA ATGTCTCCCC	480
	TGTACCAAGA TGAAGCCCT AAGGNAACAG AGGCTTCTTC GGGGACAGAA GCTGCCACTG	540
	GCCTTGAAGG GGAAGAAAAG GATGGCATCT CAGACAGTGA TAGCAGTACT AGCAKTGAGG	600
10	AAGAAGAGAG CTGGGAACCC TCCGTGGTAA GAAGCGAASC GTGGGCCTAA AGTCAGATGA	660
	TGACGGGTTT GAGATAGTGC CTATTGAGGA CCCAGCGAAA CATCGGATAC TGGACCCCGA	720
15	AGGCCTTGCT CTAGGTGCTG TTATGCGCTC TTCCAAAAAG GCCAAGAGAG ACCTCATAGA	780
	TAACCTCCTC AACCGGTACA CATTTAATGA GGATGAGGGG GAGCTTCCGG AGTGCTTTGT	840
	GCAAGAGTAA AAGCAGCACC GGATACGACA GTTGCCCTGTT GGTAAAGAAG AGGTGAGCA	900
20	TTACCGGAAA CGCTGGCGGG AAATCAATGC ACGTCCCATC AAGAAGGTGG CTGAGGCTAA	960
	GGCTAGAAAG AAAAGCAGGA TGCTGAAGAG GCTGGAGCAG ACCAGGAAGA AGGCAGAAGC	1020
25	CGTGGTGAAC ACAGTGCACA TCTNCAGAAC GAGAGAAAGT GGCACAGCTG CGAAGTCTCT	1080
	ACAAGAAGGC TGGGCTTGGC AAGGAGAAAC GGCATGTCAC CTACGTTGTA GCCAAAAAG	1140
	GTGTGGGCGG CAAAGTGCGC CGGCCAGCTG GAGTCAGAGG TCATTTCAG GTGGTGGACT	1200
30	CAAGGATGAA GAAGSACCAA AGAGCACAGC AACGTAAGGA ACAAAGAAA AAACACAARC	1260
	GGAAGTAAGC AGAGCTGCCA GGCTCCAGG AGAGCATGGG GACTAGGAGG AAGGGTGTGG	1320
35	CATGGCTCAG TCTGGCCCCC TTGATTACCG GCCTAGCCCC TGCTCACATC ACAGCTGTCT	1380
	GAACAACAGT GAGGTGGAGT GCCTAGAACT CCCGTGGTGG TCCTGAGCAG AGAGGAGGAT	1440
	GTCTCTCTGC CTGCCTGAAG GTCTCCCATG AAAACACTGC TGAAGTGTGT TGACACTCAT	1500
40	GACCCCTTTT TTAAACCGTT AAAGGGAAGT TCGGTGTGG AGCGATACTC AATGTACTCA	1560
	GTCTACACCT GGACGTGTGG GCCACTTAAG CCGTCCCCAC CCCCATCCTA TTCTTAATA	1620
45	AAACCAGGAT AATGGAAPAA AAAAAAAAAA AAAAAAAG GGGGGGCCCN TAAAGCGNCC	1680
	CANNTTT	1687

50

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 1842 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

	GGATGACAGA TTGCGACANA GATTTGTGAC CTTTCCTGCT GAACTTCAGA GGGAGCTGAA	60
	ANCAGCGTAT GATCAAAGAC AAAGGCAGGG CGAGAACAGC ACTCACCAGC AGTCAGCCAG	120
5	CGCATCTGTG CCCCAGAGAAT CTTTACTTTC ATCTAAAGGC AGCAGTGAAA GAAAAGAAAA	180
	GAAACAAGAA GAAAAAACC ATTGGTTCAC CAAAAAGCAT TCAGAGTCCT TTGAATAACA	240
10	AGCTGCTTAA CAGTCCTGCA AAAACTCTGC CAGGGGCGCTG TGGCAGTCCC CAGAAGTTAA	300
	TTGATGGGTT TCTAAAACAT GAAGGACCTC CTGCAGAGAA ACCCCTGGAA GAACTCTCTG	360
	CTTCTACTTC AGGTGTGCCA GGCCTTTCTA GTTTGCAGTC TGACCCAGCT GCCTGTGTGA	420
15	GACCTCCAGC ACCCAATCTA GCTGGAGCTG TTGAATTCAA TGATGTGAAG ACCTTGCTCA	480
	GAGAATGGAT AACTACAATT TCAGATCCAA TGGAGAAGA CATTCTCCAA GTTGTGAAAT	540
20	ACTGTACTGA TCTAATAGAA GAAAAAGATT TGGAAAACT GGATCTAGTT ATAAAATACA	600
	TGAAAAGCCT GATGCAGCAA TCGGTGGAAT CGGTTTGGAA TATGGCATT TACTTTATTC	660
	TTGACAATGT CCAGGTGGTT TTACAACAAA CTATATGGAAG CACATTAAAA GTTACATAAA	720
25	TATTACCAGA GAGCCTGATG CTCTCTGATA GCTGTGCCAT AAGTGCTTGT GAGGTATTTG	780
	CAAAGTGCAT GATAGTAATG CTCGGAGTTT TTATAATTTT AAATTTCTTT TAAAGCAAGT	840
30	GTTTTGTACA TTTCTTTTCA AAAAGTGCCA AATTTGTGAG TATTGCATGT AAATAATTGT	900
	GTTAATTATT TTAAGTATAG ATAGATTCTA TTTACAAAAT GTTTGTTTAT AAAGTTTAT	960
	GGATTTTAC AGTGAAGTGT TTACAGTTGT TTAATAAAGA ACTGTATGTA TATTTGGTAC	1020
35	RGGCTCCTTT TKGTAAYCC TTA AAAACTC AACTCTAGGA RGCAACTACT GTTTATTATA	1080
	CTAAARGGCT GAAAAMCCTC CAGGCCAGAC TGCTAAGCTC TGAAATVCC TGAAGGTCTC	1140
40	AGACCGGGAT TCTACTTGT TCAAGAAAGG GTAAGGCTC TAAACCATCT TATTTCTGTC	1200
	TCCAAGCATG AACACAGGAG CATGTAAAGA AAATCTTTAC TACTTTCTYC CATGCCGAGA	1260
	AATCTACATA TTTTGAATTA GAAACACCCT CACACCCACT TGAAGATTTT TTTCTGGGA	1320
45	ACATTATGTC CCGTAGATCA GAGGTGGTGT TGTCTTTTTC CTCTACTGG CCATTGAGAA	1380
	ACTTTGATGA TAAAAAGAA CGGTATAGAT TTTTCAAACG TATATAAAAT ATTTTATGT	1440
50	TATATGTTAT GCCATAACTT TAAAATAAAA ATAGTTTAAA ATTCTATGCT AGTGGATATT	1500
	TGGAACTTTT TCCTCAAACA AACACCCAC ACTGACTTCA GCAAAACCCT AAAACTAGCT	1560
	ACAGATTACT ACTACGAATG AATCATYAAG TTTTGTGTCT GCAACAATTT AGAAGCACTA	1620
55	AGCCCAATA TCAGGAAATG TGTGTATGAT GGAATTTTCT AGGACAAAAC AGATCAAGAT	1680
	TAAACAGGA TCAAGGATTA ATGGTATPAA AATGGTCTAC TAAACAGGA TCAAGGATTA	1740
60	AAACAGGATC AAGGATTAAT GGTATAAAAA TCTCTACTGG TTACCGGGTG GCNGGGCCAT	1800

ACAGGGTAGT GGTGGATGGA TAGTTTAGTT TGGNAAGGGT AA

1842

5

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

15

GGCAGGAGCC CTATGCTGTT CTTGTGATAA TGAGTGAGTC TCACAAGATC TGGTGGTGTT 60

ATAGGCCATCT GGCATTTCCC CTGCTGACGC TCAATTCTCTA TCCTGCCACC CTGGGAAGAA 120

20

GTGTCTTCTG TCATGATGT AAGTTTCCTG AGGCCTCCCC AGCTATGTAG AACTGTGAGC 180

CAATTAAACC TCTTTTCTCT ATAAATTATC CAGTCTTATA TATTTCTTCA TAGCAGTGTG 240

25

AGAACAGATA ATACCGTAAA TTGGTATCAC AGAGAGTGGG GTGTTGCTAT AAACACATCT 300

GAAAATGTTA AAGCAAATTT GGAAGTGGGT AACAGGCAAA GGCTGGAACA GTTGAAGAA 360

CAGTTAAGAA GAAGACAGGA AAATATGAGA AATCTTGAAA CTTCCTAGAG TCTTAAAGGT 420

30

CTCAGAAGAC ATGAAGATGT GGAAGCTTT GGAAGTTCCT AGAGACTTGT TTGAATGGCT 480

TTGACCAAAA TGCTGATAGT GATATGCACA ATGAAGTCCA GGCTGAGCTT ATCCAGACAG 540

35

ACATAAGAAG CTCGCTGGGA ACTTGAGTAA AGATCACTCT TGCTAGGCAA AGAGACTGGT 600

GGCCTTTTTT CCTCTGCCCT AGAGATCTGT GGAATCTGA ACCTGAGAGA GATGATTTAG 660

GGTATCTGGC AGAAGAAATA TCTAAGCGGC AAAACCTTCM AGAGGAAGCA GAGCATAAAC 720

40

GTTTGA AAAA TTTCAGCCT GACNATGGGA GACCAAAGTT AAACCCAAAT 770

45

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

55

GAATTCGGCA CGAGCTGAGA GGCACAGGAG CAACAGCCAG TGCCCCCTGC AGAGGACCAC 60

TGGGGTCACA GACTTCARAC CTGATGACCT GGGCTCAGAT CCCAGCTCTG CACCTACCAG 120

60

CCGTGTGACA AGGTGTCTTC TCTGAGCCTC AGTCACACAC TGCCTTAACG GTTGGGCCTC 180

ATGGAGCTGT TTGTGAAGGT TAAATGGGAA GACATAAAGC ACTTAGCCCA GAGCCAAAGGA 240  
 CATGCTGAAT ACGATAATGG TGGCCTCCTT TGGCGCTGTG CTGGTGCCAGG TGTGCCGAGG 300  
 5 AAYTGGGCAG GGGTGACAGA TACCTCTTCT AACCTAGTTC CTTTCCAAGA ACCTAATTGG 360  
 TGTCTCTCCC TCCCCAGGC AATTGGAAGG AGGAGGCTGG GCCCCAGCCC CAGAATACGG 420  
 10 GAGGTTTCTC ACCGTGGTAG GGAAATTGCT GGGTTGGGGG TGTGGGCAAC CACAGTGATC 480  
 GTCTCTCTGC AGGACGGATG AGGCTTTGCT GACAGAGGC 519

15

(2) INFORMATION FOR SEQ ID NO: 163:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

30

35

40

45

50

55

(2) INFORMATION FOR SEQ ID NO: 164:

## (i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 1400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

5	GGCAGAGTTT ATTAATACCT ATTATGCGAA AGTCACCTTC GTTGGCATTG AAAATTACAT	60
	CATCTTTAAA GCAGTATTTG TCCCCAGATG GACTCATCAC TAGCAAAGAC TAGGTTCAAT	120
10	GGAAGGCATA GGGTGAGAGA ATGGGAGCAT GAGTGGAGG CGGGTTGTTA AAGTGGTGTG	180
	AGTGAGTGAT TTTGTCTACT TGAATATCG TCCATGTTTG GGGGCATATT GTGTTTCATA	240
	AGAAGTGAAA GGTATTTGCA AGTRAGCTA CAAATGACCC ATAAATCTGT TAACAACAGT	300
15	CCTTAATATG CAAAGATGAA AAACAAACAT TACTGCTACC CAAAGGGAAC TGGTGGTTGG	360
	TGATGTGCAG ATGGGGCTGT TGGTTAAGAG AGCTATACAA GGTTCCTCTT CTTAGGTTTC	420
20	ATAGGAGSTA GTTACTGACA TGAGATTGTT TTATCTTTTT GAATACAGAT CTCTTGCTTT	480
	GAGTTAGTTC TGAGGATGGG AGTAATAAAG GAGTTTTTTG TTTTTTGTG TGTGTTTGG	540
	TTTTGGCTCC TTAGTAATAC TCCTCTGACA TTTATTTCTA TTATCTTCA AAGAAAGGAA	600
25	ACCAACTGAA ATGTTTGCTT TAACAAACAT TTAAATAGT TCTCTGGGT TTTTTTCCC	660
	CTTTTAAAAA AATTAGCATA TACCTAGCA ATAAAAGAAC TAATGTTAAC TATTGTATGC	720
30	TACAACTTAA GTGATTTTTC TAAGAAGCA CAATGTCATT GRAAGTATTA TTGAAAAGGA	780
	TCATAGTCAC ATTGAATTG TGAAGGCCAA AGAAATGAA GGGAGTGATA TTTTCATTTT	840
	ATGATATTCA CATATTTAGT AAATTTGTG TACAAGAATA CCAGGCAGAG TGTTTTACCC	900
35	ATGGAAACAG GTTTCAGATT ACTTTGTTTT TACTGTTAGA GTCTCAAGTT TAGAAATGCT	960
	AACACTTAAA TCAGTTTTTT TCTCACTATA CTTGAAGATT GTTAATATTT TGATATCTTC	1020
40	CTAGCTTGAT GGAATTTAAA CATATCTTCA GATCTGTGAC AGTGACAGCC AATAGGACTG	1080
	ATAATATTAG CTTCAACCA ATAAATGCA GGGTAAAAAT AAAATCATA GTGAAAGTAC	1140
	GATTGTAAAA TTATGCTATA TTAATTTTA AGTCTGTAAT AACTTGACAT CAAAATGTTA	1200
45	TGTAATTACC ATAAATAATG GCTAGCGAGA ACATCTTTGG AAATCTCAA ATTACCTTTC	1260
	TTACTACACT GTTTCAGAA TGATGTAGA AATGATCCTG TTAGCTTTCT GAATGTTCTG	1320
50	TGGTTGAATG TGTGTTTGCT TAAATAAGC TTTTGGTATT TGTGTTAAATW ACAAAAAAAA	1380
	AAAAAAAAAA AAAAATCGA	1400

55

## (2) INFORMATION FOR SEQ ID NO: 165:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2153 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

5	CAGGCGCTCAG GGCCTCTGGT GGCTCTGGCC CAGACAGTAT TTGCAGTTCT TGTGCTATGG	60
	GTGGGAGTCT TCTTCTCAA GTTTCGGCAG CTGTGCTGTG NCTGGATGGG CTGCTCCTCC	120
10	CAGGGCTCAA GGGCTGTGGT CCGCTCAGGG TCTCATTTCG CCAGGCCAAG TTCAAGGCAG	180
	CAGCCCTTTG TGAGGCGCTC TTGGCCCTGG GCTGGAGGGA GAACCTTAAG CTTTITTTGCT	240
15	CACAGGGAGG TGGTATGGG CCTGGGTGCA GGTGCCCACA TTCTGCTAAT GAGAGCTTTG	300
	TCTGATCAGT CCTGGGTCCA TCAGTTTGTG CATGTGTCCG GCTGCCAGCC CGTCCCTTGG	360
	GATCCTTCCC CTGGGCTGTA GCCTTGTTC ATAGTATATA CTCATTCCCT CATGCTTTCC	420
20	TCAGCAGAAC ACTTCCACTT CTGAGGTGAG CTTTGGCCCC RTGCCCTTCC TCCACAGGTG	480
	TTGCCCTTTT ATAAAGACCT GATAGCAGAA TAAATTGGTG TTCCCTGTT GACCCAGCAC	540
25	CATTTCGTG GGCCTAGAAT ATGCCCTCA ACCCTTAGAG TGGGGCAGTG AGGGCTTGAG	600
	GAGTGACCCCT TCCTTTCTCA TGGTTTAGT CATTTTGGCT GCCAGCCCTT AATGGCACAG	660
	ATCTGCTGCT TCTAACAGAT GCCCAGGAG TGACACCGAT TTCAGCCATT GCCAAGGTTA	720
30	GCACCCCTCT CTTTGAGCCT AGGCCACAC TGTTCATTGT CACTTTAGGC AAGTGCCTGT	780
	TTGGCTTTAA AGGTAAGCCT GCCAGCTGTG AGAAGCCTTG GTAACGTATG GACTCATTTT	840
35	CTGGTCCTTA AAGATGCAGC CTCTTAAGGG CTCTTGATG GATGCCATCT CTCCTAGCCC	900
	CCAGCCCTGG TGCCACTGGT GGGCAGGTC CCATTCTTTG GGGCTGGGAG GGACAGCTTG	960
	CCTGTTTCTG GTCACAAAT ACAGTCTTCT CTCTGTACC ATTCTGTGGC TTCAGCATGG	1020
40	GGGCAGTAGC CTTTCATTAG TGTAGATAGT CATCCCTGG TAGGGTGGAG GGTAAGACAT	1080
	AGGGTCTGGA ACTGTTTGGG ACCTTTTGGG GATGTCTGT GCCTCCAGA TTCCTMGATT	1140
45	CTGGGAGGAG AGGCTGCCGC ATTCTGTGC TCCTCACAGC GAGCAAAGCT GCACCCACTT	1200
	ACATTCAGTA TTTTCTGGC ACTACAAAGA GTGGGAAGGC CTGGGATTTG CTGCTGCTCC	1260
	CTTAGAGCAG GGGCCCTT TTTCAGCACTT TGGACACCTG GAGACCCAGC CCTGTTATTT	1320
50	AATGGTAGTG GGCAAGTGTG TGTGCATACT GTCTGCCACT GCTTCTCTCC TGCCCCATGC	1380
	CAGAGAGCCC TGTCCCTGCC AGGCCAGCC TTCTTAGCCC CAACTTGGGA ACAAGTGCA	1440
55	ACATGGGATC ATGGGTTGGG GTGCTCAGGT GAGCCCTCTC TATAGTGCTT CCCTGGGCA	1500
	AGCTGACACC AGCCCTGAG GGTGGGTGG GACGGGTGGT GCTTAAAAGA GGAAGGGGAC	1560
	CAGGTAGCA ACTTGCCAGG GACCCACCC CTCCCTCTCT GGGCTGTGC AGTGAGCATG	1620
60	GGGATTCCCA TCAAGGGGCC TGGCACCTGT GCTAGTTAGG TAGCCGCTGN TCACGGCTC	1680

5 ACTCCTGACC ACATGCACGT TCCCTAGATG CAGACTGCTT TGAACCTTAA AGCTGTACAA 1740  
 TTTGGTTATG TTTGTGCTGA CTTPAAATAT ATTTTAATGA GGAAAAATA ATGGAGAACC 1800  
 CTGGGAAGGA CCTGGTTCCT TTGCTTCTCG GGGAACTGTA AGCCCTCGCG TTCTGGGAAT 1860  
 CGCTCTCTGC TGCTCTTTCC TGAAGCTAA GCCTGTCTCC ACCGCCCGAG GCCTGCGCCG 1920  
 10 GTGCTCCCGC CGCAGTTGCG TTTGCTTTGG ACCTTGCCTG CGGGGGAGGG GGTGCTCGGT 1980  
 CGGAGCCCGC TCCTTTCTGT ACACCTAGCG CTGCCCGCCC CGCTTGTGTC TGAGGTGCTG 2040  
 TATGTCAAAA ATAAAGCCGC TAGAAACGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100  
 15 AAACCTCGAGG GGGGGCCCGT ACCCAATTAA CCCNMTATGA TCTATAAGC GTC 2153

20

(2) INFORMATION FOR SEQ ID NO: 156:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

35 GCGCCACGGT CCGCCACGCG GTCCGGCGGT GCGGAGTATG GGGCGCTGAT GGCCATGGAG 60  
 GGCTACTGGC GCTTCTGGC GCTGCTGGGG TCGGCACTGC TCGTGGGCTT CCTGTGGGTG 120  
 ATCTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGGAGCGCA 180  
 CTAGAGTTTA ACTGGCAGCC AGTGCTCATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC 240  
 40 GCCATCATCG TCTACAGACT GCGGTGGACC TGGAAATGCA GCAAGCTCCT GATGAAATCC 300  
 ATCCATGCAG GGTAAATGC AGTTGCTGCC ATTCTTGCAA TTATCTCTGT GGTGGCGGTG 360  
 TTTGAGAACC ACAATGTTAA CAATATAGCC AATATGTACA GTCTGCACAG CTGGGTTGGA 420  
 45 CTGATAGCTG TCATATGCTA TTTGTTACAG CTTCTTTCAG GTTTTTCAGT CTTTCTGCTT 480  
 CCGTGGGCTC CGCTTCTCT CCGAGCMTT CTCATGCCCA TACATGTTTA TTCTGGAATT 540  
 GTCATCTTTG GAACAGTGAT TGCAACAGCA CTTATGGGAT TGACAGAGAA ACTGATTTTT 600  
 50 TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCAGAAG GTGTFTTCGT AAATACGCTT 660  
 GGCCTTTGTA TCCTGGTGTT GGGGGCCCTC ATTTTGTGGA TAGTCACCAAG ACCGCAATGG 720  
 55 AAACGTCTTA AGGAGCCAAA TTCTACCATT CTTCTATCAA ATGGAGGCAC TGAACAGGGA 780  
 GCAAGAGGTT CCATGCCAGC CTACTCTGGC AACACATGG ACAATCAGA TTCAGAGTTA 840  
 AACAGTGAAG TAGCAGCAAG GAAAAGAAAC TTAGCTCTCG ATGAGGCTCG GCAGAGATCT 900

60

ACCATGTAAA ATGTTGTAGA GATAGAGCCA TATAACGTCA CGTTTCAAAA CTAGCTCTAC 960  
 AGTTTTGCTT CTCCTATTAG CCATATGATA ATTGGGCTAT GTAGTATCAA TATTTACTTT 1020  
 5 AATCACAAAG GATGGTTTCT TGAAATAATT TGTATTGATT GAGGCCTATG AACTGACCTG 1080  
 AATTGGAAAG GATGTGATTA ATATAATAA TAGCAGATAT AAATTGTGGT TATGTTACCT 1140  
 10 TTATCTTGTT GAGGACCACA ACATTAGCAC GGTGCCTTGT GCAKAATAGA TACTCAATAT 1200  
 GTGAATATGT GTCTACTAGT AGTTAATTGG ATAAACTGGC AGCATCCCTG A 1251

15

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

GACSMCTTAG AACTATGGTC CCCCCGGACT GCAGGAATTC GGCACAGCGG CTGCGGGCGC 60  
 GAGGTGAGGG GCGCGAGGTT CCCAGCAGGA TGCCCCGGCT CTGCAGGAAG CTGAAGTCAG 120  
 30 AGCCCCGGAG AGGCCCCAGC CCGCCCCGGG CAGGATGACC AAGGCCCGGC TGTTCGGCT 180  
 GTGGCTGGTG CTGGGTCGG TGTTCATGAT CCTGCTGATC ATCGTGTACT GGGACAGCGC 240  
 AGGCGCCCGG CACTTCTACT TGCACACGTC CTTCTCTAGG CCGCACACGG GCGCCCGGCT 300  
 35 GCCCAGCCCC GGGCCGGACA GGGACAGGGA GCTCACGGCC GAYTCCGATG TCGACGAKTT 360  
 TCTGGACAAK TTTCTCAGTG CTGGCGTGAA GCAGAGTGAC YTTCCACAGAA AGGAGACGGA 420  
 40 GCAGCCCGCT GCGCCGGGGA GCATGSAGGA GAGCGTGAGA RGCTACGACT GGTCCCCCGG 480  
 CGAGCCCCGG CGCACCCAGA CCAGGGCCGG CAGCARGCGG ANCGGAGGAR CGTGCTGCGG 540  
 GGCTTCTGGG CCAAYTCCAG COTGGCCTTC CCCACCAAGG AGCGCGCATT CPACGACATC 600  
 45 CCCAACTCGG AGCTGAGCCA CTTGATCGTG GACGACCGGC ACGGGGCCAT CTACTGCTAC 660  
 GTGCCCAAGG TGGCCTGCAC CAACTGGAAG CGCGTRATGA TCGTGCTGAG CGGAAGCTGT 720  
 50 GCACCGCGTG CGCTACCGC GACCCGYTGC GNTCCCGCGC GACCACGTGC ACAACGCCAG 780  
 CGCGCACTGA CTTCAACAAT TCTGGCGCGG CTACGGGAAG TCTCCCCCAG CTCATGAAGT 840  
 CAAGCTCAAG AATACACCAA TTCTTTCTGC GCGACCCTTC TG 882

55

60.

(2) INFORMATION FOR SEQ ID NO: 168:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

5 GGGAAACTCA AAAGCATGAT GGAATGGTTG ATGGAGCCAG AGCCTAGAAG TRAAGGGATA 60  
 10 CAGAGTGAAG ATAGAGGTAT TTACGTATAT TTWAATATTA GCTTTGGAAT TACGTAGGGA 120  
 TTCTTAAGAA AAGATCATGA CAGGACAGCC ACATTTGGTA AAATGTCAGG GCAGCCAGTG 180  
 15 CATGGTCCTC CTGGGGCTCC TCAGTTGACG GGTTTAAATC ATTTCTGAT CCCCCTGCCC 240  
 TGGTTTGAGG AATGCATACA GTACGTGAAA TGCCTGTGGT ATGAGTTGCA ATGGGCAATC 300  
 AACCTGGGTA AATCCAAGAT TAATGATTAG TTCTAAAGAT CCAGTTGAAG TTCTAGAGTG 360  
 20 GGAATTTTCC GTCAAGCARC TCAGCACAGC TTTATGCCTG TTCCTCTAAT AACGATAGGT 420  
 AACAAATACC TGTGKTWCA CAGCTAGGAR GATAACCAA TCTAGAGTTC TTGARTCTCA 480  
 25 TTTAATAAAT AAKTATTATG AGTACCAACT GCATATTTCA GGCCTGCTAT TTGACTCTGT 540  
 TAAATACTGA TYCCTAKGA CMSCCAGWTC AGAWAACMTT AATCTGTCTG ATCAATAAAC 600  
 AGCTTGACTT AGAGRGTA AATAGCTTGC CACAGGTWAC CCAATTAGTA GGTACACGG 660  
 30 ACAGAATAAC AGTGCAGTTA AAATCTTAGA CTGGAGACTA ATTGCATAAG TTTGAATTTT 720  
 AGTTCTGCTA TGTAAATTTG GGTGAGTACC TTAATTYACC TGAGTCTCGG TCTTTATATC 780  
 35 TGTAGAATGG AGCTAATGAT ATTACTTAAT TTGCTTTATG TGAGATTAAA TGTACTAATA 840  
 TATGTAAATC ACTTACAACA GCATTTGACA TATTTGACAT ACTTAATATA TTGCTACTA 900  
 ATACTATTAG CAACAGCATT CTGAATTTCC AAGTTGAAAT TCAGTGTMTT CTTTTTTACT 960  
 40 TTGCCATAAT TTACAATGTT GTGCTCTGTA AACCATAAAT TTCCCTGAGG TGTGTGTCAGG 1020  
 TTAAAAAATA ATCACTATGG CCCCCARNMA CTTCGAAAAT AGAAATGAGA CCAGCTTCAT 1080  
 45 CTATATTCTT TACTGCAAT AACTTAGAAT TGTAATAGGC TAATATGTAC TGGGACTTCC 1140  
 AATTTGGGAA TATGACAAAA ATAATACTAT TTAGCTAAAA CATATACAGA ACTTATTTTT 1200  
 50 CCTCTGAA 1208

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5 GCCACCAGAG AAAAGAGGTT GAGAATGTTT TCTAGCAGGC AGAATGTGCA TACATGTTTT 60  
 CATGARTGTC CTTTGGGTGC TGTTCCTTTT AAATCCTCTG TGCACAGGGC TGTGGCCTTT 120  
 ARTAAACTGT TTTTCTGTCT TACGTCATGC TGACTGGGTG CTAGGGGCTG ATTACAAAGG 180  
 10 GGAAGAGTTG AACAGACATC AGGGCCCGAT GAAACCPAAG GACTAGGAGT CAGGAGAACA 240  
 AGTCAGGGAT TAGGAGACAG CGGTTTGGTT TATGTTATC CAGCTGGAGG ACTCCTAGGG 300  
 15 GCAGCAGCAG GAGGAATACC AGGGCCACGG AGGGGCAGGA GTCTCACAGT GGAGGGCAGA 360  
 CTCTAACAGA TGCCAGCTGA ACGCTCGCTG GCCTCGATG TCATACGAGT TGGGGACCAG 420  
 AAATCTGGGC TCAGAGAACG CGTCCAGGGA GATTGGAAC CATGGGTAT CTCTAGAGT 480  
 20 TGATACTGAT AATATATTTT AATTTTATT GATGTTTAA ACCTTCTGAA ACAGGACGGT 540  
 AAGATCAGAT GGAAGCCCTT TCTGTTGAAG GATCTTGGGA ACCTTGGTGG TTTTTTTTTT 600  
 TTGGTTTTTT TTTTTTGAT CGAGCTGTGG ACATCCTTCT TAATTCGATT NTGAGGATTT 660  
 25 GTTTAACTAA AAAGTCCCA AACACAGAAA GGGCCTCCCC ACCTGCTTTG GGGAGCTGTC 720  
 TGTCTGGGA GTGCCAGGCA TCCSATGGGA CCCATCACTG CCAGTGTCTG TGCTCCCGAG 780  
 30 AGGTCAGCCC TGTGTCTGCC CTGGCTCTGT CTCTCTGTG ACAGGGCAGA GCATTTCTGG 840  
 TCAGTTCTC CATGGTGCCT CCCACCCCTT TGTAAGTGG ATGGACATGA TGAATTGAG 900  
 TTGTCTCACC CTGATAGCCT GGGTGTGAT ATTCACTTTA CCCGCACTCA GACACAGGCG 960  
 35 ACCTTGAAGC AGTTCTCGGT GTGTAGAGTC CAGTGACAG TCCCCACAGC CTCCCCAGAT 1020  
 AGCTGTGTGC CTGTGCGCTA CTGCTGTGCC ATTTTCCCAA CTNNGCGTT TCACTAAATG 1080  
 40 CAGCTGATCT CTCTCTCTGT GCACTCGTGA TCCATGTTGA ACAATACATG TAGGTTCTTT 1140  
 TTCCACGCAA TGTAAGAACA TGATATACTG TACGTTGGAA AGCATTTACC TTATTTATAT 1200  
 ACCTGAATGT TCCTACTACA CAATAAACA TATATTAAT WCTAAAAAA AAAAAAAAAA 1260  
 45 CTGGAGGGGG GGGCCGGTAC CCAATCGCC GGATAGTGAT CGTAAAC 1307

50

## (2) INFORMATION FOR SEQ ID NO: 170:

## (i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

	GGCAGGAGGT CCGCGCCGCG GCGGCTGGA ATTGTGGGAG TTGTGTCTGC CACTCGGCTG	60
	CCGGAGGCGA AGGTCCCTGA CTATGGCTCC CCAGAGCCTG CCTTCATCTA GGATGGCTCC	120
5	TCTGGGCATG CTGCTTGGGC TGCTGATGGC CGCTGCTTC ACCTTCGCCC TCAGTCATCA	180
	GAACCTGAAG GAGTTTGCCC TGACCAACCC AGAGAAGAGC AGCACCAGAG AACRGAGAG	240
10	AAAAGAAACC AAAGCCGAGG AGGAGCTGGA TGCCGAAGTC CTGGAGGTGT TCCACCGAC	300
	GCATGAGTGG CAGGCCCTTC AGCCAGGGCA GGCTGTCCCT GCAGGATCCC ACGTACGGCT	360
	GAATCTCAG ACTGGGGAAG GAGAGGCAAA ACTCCAATAT GAGGACAAGT TCCGAAATAA	420
15	TTTGAAAGGC AAAAGGCTGG ATATCAACAC CAACACCTAC ACATCTCAGG ATCTCAAGAG	480
	TGCACTGGCA AAATTCAGG AGGGGGCAGA GATGGAGAGT TCAAAGGAAG ACAAGGCAAG	540
20	GCAGCTGAG GTAAAGCGGC TCTTCGCCCC CATTCAGGAA CTGAAGAAAG ACTTTGATGA	600
	GCTGAATGTT GTCAATGAGA CTGACATGCA GATCATGGTA CGGCTGATCA ACAAGTCAA	660
	TAGTCCAGC TCCAGTTTGG AAGAGAAGAT TGCTGCGCTC TTTGATCTTG AATATTATGT	720
25	CCATCAGATG GACAATGCCG AGGACCTGCT TTCCTTTGGT GGTCTTCAAG TGGTGATCAA	780
	TGGGCTGAAC AGCACAGAGC CCCTCGTGAA GGAGTATGCT GCGTTTGTGC TGGGCGCTGC	840
30	CTTTTCCAGC AACCCCAAGG TCCAGGTGGA GGCCATCGAA GGGGGAGCCC TGCAGAAGCT	900
	GCTGGTCATC CTGGCCACCG AGCAGCCGCT CACTGCAAAG AAGAAGGTCC TGTTCGCACT	960
	GTGCTCCCTG CTGGCCCACT TCCCTATGCG CCAGCGGCAG TTCCTGAAGC TCGGGGGGCT	1020
35	GCAGGTCTTG AGGACCTGCG TGCAGGAGAA GGGCACGGAG GTGCTCGCCG TCGCGTGGT	1080
	CACACTGCTC TACGACCTGG TCACCGAGAA GATGTTGCCG GAGGAGGAGG CTGAGCTGAC	1140
40	CCAGGAGATG TCCCCAGAGA AGCTGCAGCA GTATCGCCAG GTACACCTCC TCCAGGCTT	1200
	GTGGGAACAG GGCTGGTGGG AGATCAGGGC CCACCTCCTG GCGCTGCCCC AGCATGATGC	1260
	CCGTGAGAAG GTGCTGCAGA CACTGGGCGT CCTCCTGACC ACCTGCGGGG ACCGCTACCG	1320
45	TCAGGACCCC CAGCTCGGCA GGACACTGGC CAGCCTGCAG GCTGAGTACC AGGTGCTGGC	1380
	CAGCCTGGAG CTGCAGGATG GTGAGGACGA GGGCTACTTC CAGGAGCTGC TGGGCTCTGT	1440
50	CAACAGCTTG CTGAAGGAGC TGAGATGAGG CCCCACACCA GCACTGGACT GGGATGCCGC	1500
	TAGTGAGGCT GAGGGGTGCC AGCGTGGGTG GGCTTCTCAG GCAGGAGGAC ATCTTGGCAG	1560
	TGCTGGCTTG GCCATTAAAT GGAACCTGA AGGCCAAAAA AAAAAAAAAA AAAAAAAAAA	1620
55	AAAA	1624

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2003 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

10 GGCACGAGCC AGCTTGCAGG AGGAATCGGT GAGGTCCTGT CCTGAGGCTG CTGTCCGGGG 60  
 CCGGTGGCTG CCTCAAGGT CCTTCCCTA GCTGCTGCGG TTGCCATTGC TTCTTGCTTG 120  
 TTCTGGCATC AGGCACCTGG ATTGAGTTGC ACAGCTTTGC TTTATCCGGG CTTGTGTGCA 180  
 15 GGGCCCGGCT GGGCTCCCCA TCTGCACATC CTGAGGACAG AAAAAGCTGG GTCTTGCTGT 240  
 GCGCTCCAG GCTTAGTGTT CCTCCCTCA AAGACTGACA GCCATCGTTC TGCACGGGGC 300  
 20 TTTCTGCATG TGACGCCAGC TAAGCATAGT AAGAAGTCCA GCCTAGGAAG GGAAGGATTT 360  
 TGGAGGTAGG TGGCTTTGGT GACACACTCA CTTCTTTCTC AGCCTCCAGG ACACTATGGC 420  
 CTGTTTTAAG AGACATCTTA TTTTCTAAA GGTGAATTCT CAGATGATAG GTGAACCTGA 480  
 25 GTTGACAGATA TACCAACTTC TGCTTGATTT TCTTAAATGA CAAAGATTAC CTAGCTAAGA 540  
 AACTTCCTAG GGAAGTAGGG AACCTATGTG TTCCCTCAGT GTGGTTTCCT GAAGCCAGTG 600  
 30 ATATCGGGGT TAGGATAGGA AGAACTTTCT CGGTAATGAT AAGGAGAATC TCTTGTTTCC 660  
 TCCCACCTGT GTTGTAAGA TAACTGACG ATATACAGGC ACATTATGTA AACATACACA 720  
 CGCAATGAAA CCGAAGCTTG GCGGCCTGGG CGTGGTCTTG CAAATGCTT CCAAAGCCAC 780  
 35 CTTAGCCTGT TCTATTCAGC GGCAACCCCA AAGCACCTGT TAAGACTCCT GACCCCAAG 840  
 TGGCATGCAG CCCCATGCC CACCGGACG TGGTCAGCAC AGATCTTGAT GACTTCCCTT 900  
 40 TCTAGGGCAG ACTGGGAGGG TATCCAGGAA TCGGCCCTG CCCCACGGGC GTTTTCATGC 960  
 TGTACAGTGA CCTAAAGTTG GTAAGATGTC ATAATGGACC AGTCCATGTG ATTTCAGTAT 1020  
 ATACAACCTCC ACCAGACCCC TCCAACCCAT ATAACACCCC ACCCCTGTTT GCTTCTGTGA 1080  
 45 TGGTGATATC ATATGTAACA TTTACTCCTG TTTCTGCTGA TGTGTTTTTT AATGTTTTGG 1140  
 TTTGTTTTTG ACATCAGCTG TAATCATTCG TGTGCTGTGT TTTTATTAC CTTTGGTAGG 1200  
 50 TAATTAGACTT GCACTTTTTT AAAAAAGGT TTCTGCATCG TGAAGCATT TGACCCAGAG 1260  
 TGAACCCGT GGCCTATGCA GGTGGATTCC TTCAGGTCTT TCCTTTGGTT CTMTGAGCAT 1320  
 CTTTGCTTTT ATTCGTCTCC COTCTTGGT TCTCCAGTTC AAATTATGTC AAAGTAAAGG 1380  
 55 ATCTTTGAGT AGGTTCCGTC TGAAAGGTGT GGCCTTTATA TTTGATCCAC ACACGTTGGT 1440  
 CTTTTAACCG TGCTGAGCAG AAAACAAAAC AGGTTAAGAA GAGCCGGGTG GCAGCTGACA 1500  
 60 GAGGAAGCCG CTCAAATACC TTCACAATAA ATAGTGGCAA TATATATATA GTTTAAGAAG 1560

5 GCTCTCCATT TGGCATCGTT TAATTTATAT GTTATGTTCT AAGCACAGCT CTCCTCTCCT 1620  
 ATTTTCATCC TCGAAGCAAC TCAAAATATT TAAATAAAG TTTACATTGT AGTTATTTTC 1680  
 AAATCTTTGC TTGATAAGTA TTAAGAAATA TTGGACTTGC TCCCGTAATT TAAAGCTCTG 1740  
 TTGATTTTGT TTCCGTTTGG ATTTTIGGGG GAGGGGAGCA CTGTGTTTAT GCTGGAATAT 1800  
 10 GAAGTCTGAG ACCTTCCGGT GCTGGGAACA CCAAGAGTT GTTGAAAGTT GACAAGCAGA 1860  
 CTGCCCATGT CTCTGATGCT TTGTATCAAT CTTGAGCAAT CGCTCCGTCC GTGGACAATA 1920  
 AACAGTATTA TCAAGAGAA AAAAAAAAAA AAAAAACTCG NGGGGGGGCC CGGTACCCAA 1980  
 15 TTCCGCCCTAT AGTGAGCCNA TTC 2003

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

30 GGCACGCGG CAGCAGAAGA CTTTGGTGTT TAAGAGATTA ATGTGTTAGC CAGAACAAC 60  
 CATTTCTCTA CCMGTGTGTA GTCCATTAT CTTTAAAGAT TTTCTATTGG AATAATTTG 120  
 35 AAATTACTTT CTTAGTTTTT TTCATTAAAA ACTAAGAAAA TGCTTTGTTT ATTATGAATT 180  
 GCTATTTCTC TTGATTATTA TTCTTGGAGA AAGTCTATCA GACGTAATTC TTCTGATTG 240  
 40 CTTCTAGGCT AGAGGAAAAT GTGAAAGATG ACAAATGAAA ATTTCAAAGG TTGTCAGTAG 300  
 TATGACTTCT TTTATCGTTT GTCAATTATCA CAAATATATC AACATAGGAC TTTTAAAAGA 360  
 TATTTTGTAC ATATTGGCCC TTAGTAGGAT TTTGCATGAA TTTTTTTTTT CTTTATGCC 420  
 45 CAGAGAGAAA GAGCAAAGAA ATAACCAAGG GTGATGTACT CGTATTGAAG GTTTACCAA 480  
 TAAGGACTGC TTTTATTATG AACTATAGTC TATATTCTAA GTAAATCAAT TTTTCTATTA 540  
 TGTGTTTTTT GTTCCTGCAG GCAAGATCTC TGAACTTTAT GCAGAGGGTT CTTTAAAAA 600  
 50 AACAAAGTTG AATTTTTTTA TTCTTGGAA TATTTTTTTT CATTGATTC TCCCAAGTAG 660  
 AGCAGATTCA AATCTCCTTT GTACCCTATG TCTTTTTTCT TTIGCTATTA GCTCAGTATT 720  
 55 CCGTTTCTAC ATTTTCCTTT CCTAGAACCA GTCAATAAAT GACAAAAAA AAAAAAAAAA 780  
 ACTCGA 786

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

5	GGGACGAGCC CTGCCACCT CCTGCAGCCT CCTGCCGCC GCGAGCTGG CGGATGGAGC	60
10	TGCGCACGGG GAGCGTGGG AGCCAGGCGG TGGCGCGAG GATGGATGGG GACAGCCGAG	120
15	ATGGCGGCGG CGGCAAGGAC GCCACCGCGT CGGAGGACTA CGAGAACCTG CCGACTAGCG	180
20	CCTCCGTGTC CACCCACATG ACAGCAGGAG CGATGGCCGG GATCCTGGAG CACTCGGTCA	240
25	TGTACCCGGT GCACTCGGTG AAGACACGAA TGCAGAGTTT GAGTCCAGAT CCCAAAGCCC	300
30	AGTACACAAG TATCTACGGA GCCCTCAAGA AAATCATGCG GACCGAAGCT TCTGGAGGCC	360
35	CTTGGGAGGC GTCAACGTCA TGATCATGGG TGCAGGCCCR GCCCATGCCA TGTATTTTGC	420
40	CTGCTATGAA AACATGAAAA GGACTTTAAA TGACGTTTTC CACCACCAAG GAAACAGCCA	480
45	CCTAGCCAAC GGTATTTTGA AAGCGTTTGT CTGGAGTTAG AAAGTTCTCT TCTTCAACAC	540
50	GTCCCTCCCG AGGGTGTTC TCCCTGTGAC CCAGCCGCC CTGACTTCGGC CCGCTTGCTC	600
55	ACGAATAAAG AACTCAGAGT TGTGTGTGCA ATGCACACCC AGACACACGC ACCACACAC	660
60	ACGGCGCGGC ACACACATGC TTTTCTCTGT TCCCCTCCGC TTTCTGAAGC CTGGGGAGAA	720
65	ATCAGTGACA GAGGTGTTTT GGTTTTATTG TTATGTGGGT TTTCTTTTGT ATTTTTTTTG	780
70	TTTGTTTTGT TTTTAAACAT TCAAAAGCAA TTAATGATCA GACATAGGAG AAACCTGAA	840
75	TAGAAACAAA ACTTTTGAAT GCTGGATTCA AAAAAAAAAA AAAGTTATCT GGACAGCTTC	900
80	TTTGAGACTA TTTAAAACT GGTACAACAG GTCTCTACAA CGCCAAGATC TAACTAAGCT	960
85	TTAAAAGGTC AAGAAGTTTT ATGGCTGACA AAGGACTCGC GCAACGCAGA AGGCCTTTCC	1020
90	CACCTTAAGC TTCCGGGGAT CTGGGAATTT TACCCCATTT CTCTTCTGTT TGTCTGAGTC	1080
95	TCATCTCTCT GCAAGCAAGG GCTGAAATCA TTTTGTTTGG TTGTTTTGAG GGAGAGAGGC	1140
100	GGGGTGGGGG GGTGCAAAATC TGCCAGCAGC TCTTACGTAA GGCATGTTTT ATGGGGAGG	1200
105	GCTGAGCTTT TATTTTCTCC TCTCCAGTGG GGTGGCTTT TATTGTTTCT TGTTTGGGTT	1260
110	TGGAATGGAA ATATGGATAG CAGCATAAAG TACTTTTATT TTGACAAAAT TCATTTTTTT	1320
115	CAACAATGGA GACATAGATT TGACCCACAA TAACTTCTCC CCTCTCTTT TACTCTGCT	1380
120	CAAAAAGCAT CTCTCTCCC ATTACCCAAC CTGGGTGATA AGTGTGCTG GCTGGTTTGC	1440
125	AGATATTTGT TCTGCTTTGT AAAAATTGGC CATTAGTGCA TTTATTGAGA TGATCTCTAA	1500

AGAGCTATGC CCTGACCTAC CCCTGATTCT ATGACATGCG GGGCCTTCTT TTGCTGAAAC 1560  
 TGCCTTACGT AATGGTTTTA CTCCTTGAAA GAGATTTGAC GGAATCCATT TTATGCCAAG 1620  
 5 TGCTGCCCTG CACTGTTTCT GCAATATGTG GTGATGCTG TGGTGATCTT GCTGGGAATG 1680  
 ATTATAAGTG TGTGTGTGGT GGGGGAGTGG GTATTACATG CATTGCTGAA GAGTCAAAAA 1740  
 10 AAAAAAAAAA AAACCTCGA 1758

15 (2) INFORMATION FOR SEQ ID NO: 174:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

25 CTGTTAGAAT GCCCAGTTTA COTGGATGGC AACCCAACAG TGCTCCTGCC CACCTGCCCC 60  
 TCAATCCTCC TAGAATTCAG CCCCCAATTG CCCAGTTACC AATAAAAACT TGTACACCAG 120  
 CCCCAGGGAC AGTCTCAAAT GCAATCCAC AGAGTGASMC ACCACCTCGG GTAGAATTTG 180  
 30 ATGACAACAA TCCCTTTAGT GAAAGTTTTT AAGAACGGGA ACCTAAGGAA CGTTTACGAG 240  
 AACAGCAAGA GAGACAACGG ATCCAACCTA TGCAGGAGGT AGATAGACAA AGAGCTTTGC 300  
 35 AGCAGAGGAT GGAAATGGAG CAGCATGGTA TGGTGGGCTC TGAGATAAGT AGTAGTAGGA 360  
 CATCTGTGTC CCAGATTCCC TTCTACAGTT CCGACTTACC TTGTGATTTT ATGCACCTC 420  
 TAGGACCCCT TCACCACTCT CCACAACACC AACAGCAAT GGGGCAGGTT TTACAGCAGC 480  
 40 AGAATATACA ACAAGGATCA ATTAATTCAC CCTCCACCCA AACTTTCATG CAGACTAATG 540  
 AGCGAGGCAG GTAGGCCCTC CTTCATTTGT TCCTGATTCA CCATCAATCC CTGTTGGAAG 600  
 45 CCCAAATTTT TCTTCTGTGA AGCAGGGACA TGGAAATCTT TCTGGGACCA GCTTCCAGCA 660  
 GTCCCCAGTG AGGCCTTCTT TTACACCTGC TTTACCAGCA GCACCTCCAG TAGCTAATAG 720  
 CAGTCTCCCA TGTGGCCAAG ATTCTACTAT AACCCATGGA CACAGTTATC CCGGATCAAC 780  
 50 CCAATCGCTC ATTCAGTTGT ATTCTGATAT AATCCAGAG GAAAAAGGGA AAAAAAARA 840  
 AMAAFAARA ARAAAGGAGA TGATGATGCA GAATCCACC AAGGCTCC 888

55

(2) INFORMATION FOR SEQ ID NO: 175:

60 (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

	GGCAGAGCTA GTGTGGACTC CATCCCCCTG GAGTGGGATC ACGNCTATGA CCTCAGTCGG	60
10	GACCTGGAGT CTGCAATGTC CAGAGCTCTG CCCTCTGAGG ATGAAGAAGC TCAGGATGAC	120
	AAAGATTTCT ACCTCCGGGG AGCTGTTGSC TTATCAGGGG ACCACAGTGC CCTAGAGTCA	180
	CAGATCCGAC AACTGGGCAA AGCCTGGATG ATAGCCGCTT TCAGATACAG CAAACCGAAA	240
15	ATATCATTCG CAGCAAACT CCCACGGGGC CGGAGCTAGA CACCAGCTAC AAAGGCTACA	300
	TGAAACTGCT GGGCGAATGC AGTAGCAGTA TAGACTCCGT GAACAGACTG GAGCACAAC	360
20	TGAAGGAGGA AGAGGAGAGC CTCCTGGCT TTGTAACTT GCATAGTACC GAAACCCAAA	420
	CGGCTGGTGT GATTGACCGA TGGGAGCTTC TCCAGGCCCA GGCATTGAGC AAGGAGTTGA	480
	GGATGAAGCA GAACCTCCAG AAGTGGCAGC AGTTTAACTC AGACTTGAAC AGCATCTGGG	540
25	CCTGGCTGGG GGACACGGAG GAGGAGTTGG AACAGCTCCA GCGTCTGGAA CTCAGCACTG	600
	ACATCCAGAC CATCGAGCTC CAGATCAAAA AGCTCAAGGA GCTCCAGAAA GCTGTGGACC	660
30	ACCGCAAAGC CATCATCCTC TCCATCAATC TCTGCAGCCC TGAGTTCACC CAGGCTGACA	720
	GCAAGGAGAG CCGGGACCTG CAGGATCGCT TGTGGCAGAT GAATGGGGGC TGGGACCGAG	780
	TGTGCTCTCT GCTGGAGGAG TGGCGGGGCC TGCTGCAGGA TGCCCTGATG CAGTGCCAGG	840
35	GTTTCCATGA AATGAGCCAT GGTTCCTTC TTATGCTGGA GAACATTGAC AGAAGGAAAA	900
	ATGAAATTGT CCTATTGAT TCTAACCTTG ATGCAGAGAT ACTTCAGGAC CATCAAAAC	960
40	AGCTTATGCA AATAAAGCAT GAGCTGTTGG AATCCCACT CAGAGTAGCC TCTTTGCAAG	1020
	ACATGTCTTG CCAACTACTG GTGAATGCTG AAGGAACAGA CTGTTTAGAA GCCAAAGAAA	1080
	AAGTCCATGT TATTGGAAAT CGGCTCAAAC TTCTCTTGAA GGAGGTCAGT CGTCATATCA	1140
45	AGGAACTGGA GAAGTTATTA GACGTGTCAA GTAGTCAGCA GGATTGTCT TCCTGGTCTT	1200
	CTGCTGATGA ACTGGACACC TCAGGGTCTG TGAGTCCCAV ATCAGGAAGG AGCACCCCAA	1260
50	ACAGACAGAA AACGCCACGA GCCAAGTGTA GTCTCTCACA GCCTGGACCC TCTGTGAGCA	1320
	GTCCACATAG CAGGTCCACA AAAGGTGGCT CCGATTCTTC CCTTTCTGAG CCARGGCCAG	1380
	GTGGGTCCGG CCGCGGCTTC CTGTTGAGAG TCCTCCGAGC AGCTCTTCCC CTTGAGCTTC	1440
55	TCCTGCTCCT CCTCATCGGG CTTGCGTGCC TTGTACCAAT GTCAGAGGAA GACTACAGCT	1500
	GTGCCCTCTC CAACAACCTT GCCCGGTCAT TCCACCCCAT GCTCAGATAC ACGAATGGCC	1560
60	CTCCTCCACT CTGAACTAAG CAGATGCCAT CTGCAGAAGT GCTGGTAGCA TAAGGAGGAT	1620



5 CCGGTCATAA GCAATCCCAA ACTACCAACA AGAGGACCTT GATCTTGGCG AAAGCCMTCC 1680  
 GTGTGGCAGC TTTAGCCTCC TCCAGATCAC ATGTGTGCAA ATTATGCCTT CAGAGGTGGA 1740  
 AGATAAACAG TGACGGGGGA ACAACAGAC AACAGAGG TTTGGAAGAA ATCTGGTTTG 1800  
 AGACTCTGAA CCTTAGCACT AAGGAGATTG AGTAAGGACC TCCAAAGTTC CCCGCACTCA 1860  
 10 TGAATCTCGG GCCCTTGGCC NATTCCTGTG ACAGCCAGG ACTTCAGTAG ACCATCTGGG 1920  
 CAGCTTTCCC ATGGTGTGTC TCCAACCATC AGATAAATGA CCCTCCCAAG CACCATGTCA 1980  
 GTGTCTGACA ATCTACCAAC CAACCAGTGC TGAAGAGATT TTAGAACCTT GTAACATACA 2040  
 15 ATTTTAAAGA GCTTATATGG CAGCTTCCTT TTTACCTTGT TTTCTTTGG GGCATGATGT 2100  
 TTTAACCTTT GCTTTAGAAG CACAAGCTGT AAATCTAAAA GGCACCTTTT TTTAGAGGTA 2160  
 20 TAAAGAAAAA CTAGATGTAA TAAATAAGAT CATGGAAGGC TTTATGTGAA AAAAGTTGAA 2220  
 TGTTATAGTA AAAAAAAG ATATTTATGT ATGTACAGTT TGCTAAAGCC AAGTTTTGTT 2280  
 TGTATGATT TCTTTGCATT TATTATAGAT ATTATAAAT AAAAAAAAAA AAAAAAAAC 2340  
 25 TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGTGAG 2379

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

40 GCGCCTTCAC GATGCGGGCG GTCAGTGGTC CAGGTCCCTT ATTCTGCCTT CTCTCTCTGC 60  
 TCCTGGACCC CCACAGCCCT GAGACGGGGT GTCTCTCTCT ACCGAGGTTT GAGTACAAGC 120  
 45 TCAGCTTCAA AGGCCCAAGG CTGGCATTGC CTGGGGCTGG AATACCCCTC TGGAGCCATC 180  
 ATGGAGGTGA GGGGCAGGGG TGGGGACCGC TATGCCCAGG GTCCCTCAA GTGCTGGAGG 240  
 50 GGCTGTRACT TGGTGGGGAG TGGGTCTGTC ACAGCCATCC TCTGTCCAG GTGGGGCAAG 300  
 GCTTGGGACA GTGCCAGGCA CCCCAGGACC CCTTCCAGGC TTGTCTCTCT CTCCACCGCC 360  
 TCAACACCCC CCACCCCTGC CCAAGCTGTT TCTCTCTGTC CTCTCTNNTT CCCTGCCCCA 420  
 55 GGACTTCTCT CTCTCTCTCT GCCTCTCCTT GGACCCCTGC CCTTCTCTTA CCTCTGACCT 480  
 GTGAACACAC AGACACATGC TCACACACTA AGTCCCARGC ACACMSAAG GCATGTGGA 540  
 60 CCAGCACAAA CCTCCACTCT CCGGGCTCCA TCCCACGGG CCTGTGGCTG GCCATGAAAA 600

CTGGGGGCTA CCTGGAGGGA AGCATCCTCA TCCCAGGTGA GTGGGCACCA GCCCTTCCCT 660  
 GTATGTGTGT TGTGGGTGGA AGCAGGCATG AGAGCATCTT AGCCCATAGG TTTGTATTCA 720  
 5 GGGACTTTCCA AACCCAGACC TACAAAGAGT GTGTCTTCTA CCAGATCTTG TTCAAAAAG 780  
 GGTTTGTGAT GATGGAATA CACGATAGAG GGAGTGAGCA AGAACAAATCA GGATTAGAGT 840  
 10 GGAGCGTGAA ATAGTCTAGG ACCATGGCTT CCAAAACATA TGCTGTGAGG TCTGTCCACC 900  
 TGAGAGTTGG GCCATGGATT TAATCTGAG CCTCTTAGCA GGCAAAGCA AGACAGAAAG 960  
 CAGATCGGCT GTGGATTCT GTCTATAAAA TGTGAGTTCT TGGCCGGGTG CCGTGCCTCA 1020  
 15 CGCCTGTAAT CCGCCGCTT TGGGAGGCCA GGGCGGATGG GTCCCGAGGT CAGGAGGTTG 1080  
 GAAACCATCC TGGCCGGAAT GGTGAAGCCC TGACTCTACT AGAAGTGCA AGATTGGCTG 1140  
 GGTGTGGTGG CCGCCGCTG TGGTCCCAGC TTCTCGGGAG GCTGAGGCGG GAGACTTGCT 1200  
 20 TGGGCTGGG AGGCCGAGGT TGGGTGAGC TGAGATCCTG CCATGCACT TCAGCCTGGG 1260  
 CACAGAGCCA GACTCTGGCT CAAAAA AAAA AAAA ACTCGAGGG GGGCCGTACC 1320  
 25 CAATTGCGCG NATATGATCG TAAACAT 1348

30 (2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

40 CTCAAAATAA ATAAATAAAT AAAAATTGT ATTCCATTGA TTTGGGTAGA CACCAGGAAT 60  
 GTGCATTCTT AACAGCTTT CCAGGCGATC CTATAGTAAG TCATCTGTGG ACTACTTTAA 120  
 45 GAAACTCTTC TATAGAGAAT GAGTTGGAT TAATAATAGG TGATTTTTTA CACTGGACTG 180  
 ATTCACAAGA ACCTAAACAG TAGTCCATGA AGCTGCTCAT CTGTGGTAAC TATTTGGCCC 240  
 CGTCTCACTC TGAAAGCAGC AGGAGATGTT GTTTACTTTG TTTCTATCCC CTTGTCTGG 300  
 50 AGATTAATTT TGAATGAAA GTTTTCTCT CTATGCCATT CCTGTTCTT TTCCAAAGCC 360  
 TCATACAAGA GGATTAGTC ACAATGCATG CATTACCTTT TAAAAGAATG CGATATTGAT 420  
 55 ACCGATGCTT ACTTTTTTTT TTTTNACTA CTGTGTTTAT TCCTCCAGN AAAGTATAGC 480  
 CCGCCTTTCT ATAGCATAGT TCTCTTAGG TGGAATGATT CCTATAAGAT TTCTCATTAT 540  
 TAAATCATGC ATTTTTCAAG ATGGAATCAA TMTTGATTT AATCTAAGCT GATATTCTCA 600  
 60 TTTGTTAGAA GAACAACCTA CATGCTAGAG AGAGAGGAGG AAATATACCC ACGAACCAC 660

AGCCAGTTAG TATCCAGTTG GTGCTGGACT CCAGCCAGGT GTCCTGCCTC ATGGTAGTTA 720  
 AATGATATAT AGAAAAGCTA AATTTTAA GAAATATTTA TTAATATATT CCTATAAAAC 780  
 5 ATTTTAAAGG TAACCACATA AAAATGCTTA ATTTTTCAT TCCAAAGTAA ATGCTAAGCA 840  
 TGTTTATTA TGAAGCAGTA CTTCTGATTA GTATATGACA TTCTGAAGTT AATTAAACTC 900  
 10 ATTGCACTAA ATGTGCTTC CTTGGTATAG TGGAGGATTT GAGGATTGGA ATATAGAGTA 960  
 GAGTGCTTGC TTAAGCCTGG GAGCCCATCT TTATAGCTAT TTGATGTAAG AAAAGAGACA 1020  
 TGGNCCATTT CTAAGCTATA TAAGGTGAGT GTGTCTATTC CCAGCAGATA TAAAGGAAAA 1080  
 15 AGGAAACTTT TTTGATTCCT ACCTTCCGAG CCTCACCTAG CCATCTTCCA GCCTCAAATA 1140  
 TAGAGATGTT AGTGCAAGGT CCTGGGCTCT AGGTGATCAT TTCATAAGTC CTTTACAGAT 1200  
 20 AAAGAAAAAG TAGTGTGTGT ATGTTTGT TTAAGTAACC CCAAAACAAA TTTATATTGT 1260  
 ATTCAGCAAA ATTGGAATTC AGGTGTTTAA TTTTACAACA TGAAGTGCCT GCTGTTTTAA 1320  
 GCATTGACTT GTATAAAAAG AATTGCATGT CTCCAGTAAG CTTATGGGTT TTCTCATTTT 1380  
 25 TAGGTATATG CTTTTTAATC ATGTAAAGTG AAACATTAGT TTTCTTGCAT TTTATTACAG 1440  
 GTTCTTTGTT GCAATAAAGA TGCTGCTGAA ATTAATTGAA AAAAAAAAAA AAAAAAACTC 1500  
 30 GA 1502

35 (2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1637 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

45 ATTTTCTAGC CCACAGGAC TGAAGTTCAG ATCCAAAAGT TCACCTTGCTA ATTATCTTCA 60  
 CAAAATGGA GAGACTTCTC TTAAGCCAGA AGATTTTGAT TTTACTGTAC TTTCTAAAAG 120  
 GGTATCAAG TCAAGATATA AAGACTGCAG CATGGCAGCC CTGACATCCC ATCTACAAAA 180  
 50 CCRAAGTAAC AATTCAAACCT GGAACCTCAG GACCCGAAGC AAGTGCAAAA AGGATGTGTT 240  
 TATGCCGCCA AGTAGTAGTT CAGAGTTGCA GGAGAGCAGA GGACTCTCTA ACTTTACTTC 300  
 55 CACTCATTTG CTTTTGAAAG AAGATGAGGG TGTGTGATGAT GTTAACTTCA GAAAGGTTAG 360  
 AAAGCCCAA GGAAAGGTGA CTATTTTGAA AGGAATCCCA ATTAAGAAAA CTAAAAAGG 420  
 ATGTAGGAAG AGCTGTTTCA GTTTTGTTT AAGTGATAGC AAAAGAGAAT CTGTGTGTAA 480  
 60

	TAAAGCAGAT GCTGAAAGTG AACCTGTTGC AAAAAAAGT CAGCTTGATA GAACTGTCTG	540
	CATTTCTGAT GCTGGAGCAT GTGGTGAGAC CCTCAGTGTG ACCAGTGAAG AAAACAGCCT	600
5	TGTAAAAAAA AAAGAAAGAT CATTGAGTTC AGGATCAAAT TTTTGTCTG AACAAAAAAC	660
	TTCTGGCATC ATAAACAAAT TTTGTTTCAGC CAAAGACTCA GAACACAACG AGAAGTATGA	720
10	GGATACCTTT TTAGAATCTG AAGAAATCGG AACAAAAGTA GAAGTTGTGG AAACGAAAGA	780
	ACATTTGCAT ACTGACATTT TAAACGTGG CTCTGAAATG GACAACAACCT GCTCACCAAC	840
	CAGGAAAGAC TTCACTGAAG ATACCATCCC ACGGAACACA GATAGAAAGA AGGAAAACAA	900
15	GCCTGTATTT TTCCAGCAA TATAACAAAG AAGCTCTTAG CCCCCACGA CGTAAAGCCT	960
	TTAAGAAATG GACACCTCCT CGGTCACCTT TTAATCTCGT TCAAGAAACA CTTTTCATG	1020
20	ATCCATGGAA GCTTCTCATC GCTACTATAT TTCTCAATCG GACCTCAGGC AAAATGGCAA	1080
	TACCTGTGCT TTGGAAGTTT CTGGAGAAGT ATCCTTCAGC TGAGGTAGCA AGAACCGCAG	1140
	ACTGGAGAGA TGTTGTCAGAA CTCTTAAAC CTCTTGCTCT CTACGATCTT CCGGCAAAAA	1200
25	CCATTGTCAA GTTCTCAGAT GAATACCTGA CAAAGCAGTG GAAGTATCCA ATTGAGCTTC	1260
	ATGGGATTGG TGCACCCTGA AGACCACAAA TTAATAAAT ATCATGACTG GCTTTGGGAA	1320
30	AATCATGAAA AATTAAGTCT ATCTTAACT CTGCAGCTTT CAAGCTCATC TGTATGCAT	1380
	AGCTTTGCAC TTCAAAAAAG CTTAATTAAG TACAACCAAC CACCTTTCCA GCCATAGAGA	1440
	TTTTAATTAG CCCAACTAGA AGCCTAGTGT GTGTGCTTTC TTAATGTGTG TGCCAATGGT	1500
35	GGATCTTTGC TACTGAATGT GTTTGAACAT GTTTTGAGAT TTTTTTAAAA TAAATTATTA	1560
	TTTGACAACA ATCCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1620
40	AAAAAAAAAA AAAAAA	1637

45 (2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2911 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

55	GGTGGTTTTT GTTCTGCAAT AGGCGGCTTA GAGGGAGGGG CTTTTTCGCC TATACCTACT	60
	GTAGCTTCTC CACGTATCGA CCTTAAAGGC TACTGCTGCT ACTACGGGGC TAGACAGTTA	120
	CTGTCTCAGC TCTAGGATGT GCGTTCTTCC ACTAGAAGCT CTCTGAGGG AGSTAATTAA	180
60	AAAACAGTGG AATGGAAAAA CAGTGCTGTA GTCATCCTGT AATATGCTCC TTGTCAACAA	240

	TGTATACATT CCTGCTAGGT GCCATATTCA TTGCTTTAAG CTCAAGTCGC ATCTTACTAG	300
5	TGAAGTATTC TGCCAATGAA GAAAACAAGT ATGATTATCT TCCAACTACT GTGAATGTGT	360
	GCTCAGAACT GGTGAAGCTA GTTTCTGTG TGCTTGTGTC ATTCTGTGTT ATAAAGAAAG	420
	ATCCTCAAAG TAGAAATTTG AATATGCTT CCTGGAAGGA ATTCTCTGAT TTCATGAAGT	480
10	GGTCCATTC TGCTTTCTT TATTTCCTGG ATAACCTGAT TGTCTTCTAT GTCTGTCTCT	540
	ATCTTCAACC AGCCATGGCT GTTATCTTCT CAAATTTTAG CATTATAACA ACAGCTCTTC	600
15	TATTTCAGGAT AGTGTCTAAG ANGCGTCTAA ACTGGATCCA GTGGGCTTCC CTCCTGACTT	660
	TATTTTGTG TATTGTGGCC TTGACTGCCG GGAATAAAC TTTACAGCAC AACTTGGCAG	720
	GACGTGGATT TCATCAGGAT GCCTTTTTCA GCCCTTCCAA TTCCTGCCCT CTTTTCAGAA	780
20	ATGAGTGTCC CAGAAAAGAC AATTGTACAG CAAAGGAATG GACTTTTCCT GAAGCTAAAT	840
	GGAACACCAC AGCCAGAGTT TTCAGTCACA TCCGTCTTGG CATGGGCCAT GTTCTTATTA	900
25	TAGTCCAGTG TTTTATTTCT TCAATGGCTA ATATCTATAA TGAAAAGATA CTGAAGGAAG	960
	GGAACCAGCT CACTGAARGC ATCTTCATAC AGAACAGCAA ACTCTATTTT TTTGGCATT	1020
	TGTTTAATGG GCTGACTCTG GGCCTTCAGA GGAGTAACCG TGATCAGATT AAGAACTGTG	1080
30	GATTTTITTA TGGCCACAGT GCATTTTCAG TAGCCCTTAT TTTGTAACT GCATTCCAGG	1140
	GCCTTTCAGT GGCTTTCATT CTGAAGTTCC TGGATAACAT GTTCCATGTC TTGATGGCCC	1200
35	AGGTTACCAC TGTCAATATC ACAACAGTGT CTGTCTGGT CTTTGACTTC AGGCCCTCCC	1260
	TGGAATTTTT CTGGAAGCC CCATCAGTCC TTCTCTCTAT ATTTATTTAT AATGCCAGCA	1320
	AGCCTCAAGT TCCGGAATAC GCACCTAGGC AAGAAAGGAT CCGAGATCTA AGTGGCAATC	1380
40	TTTGGGAGCG TTCCAGTGGG GATGGAGAAG AACTAGAAAG ACTTACCAA CCCAAGAGTG	1440
	ATGAGTCAGA TGAAGATACT TTCTAACTGG TACCCACATA GTTTGCAGCT CTCTTGAACC	1500
45	TTATTTTCAC ATTTTCAGTG TTTGTAATAT TTTCTTTTC ACTTTGATAA ACCAGAAATG	1560
	TTTCTAAATC CTAATATTCT TTGCATATAT CTAGTACTC CCTAAATGGT TCCATCCAAG	1620
	GCTTAGAGTA CCCAAAGGCT AAGAAATTCT AAAGAACTGA TACAGGAGTA ACAATATGAA	1680
50	GAATTCATTA ATATCTCAGT ACTTGATAAA TCAGAAAGTT ATATGTGCAG ATTATTTTCC	1740
	TTGGCCTTCA AGCTTCCAAA AACTTGTA TAATCATGTT AGCTATAGCT TGTATATACA	1800
55	CATAGAGATC AATTTGCCAA ATATTCACAA TCATGTAGTT CTAGTTTACA TGCCAAAGTC	1860
	TTCCCTTTTT AACATTATAA AAGCTAGGTT GTCTCTTGAA TTTTGAGGCC CTAGAGATAG	1920
	TCATTTTGCA ACTAAAGAGC AACGGGACCC TTTCTAAAA CGTTGGTTGA AGGACCTAAA	1980
60	TACCTGCCCC TACCATAGAT TTGGGATGAT GTAGTCTGTG CTAAATATTT TGCTGAAGAA	2040

GCAGTTTCTC AGACACAACA TCTCAGAATT TTAATTTTTA GAAATTCATG GGAAATTGGA 2100  
 TTTTGTATAT AATCTTTTGA TGTTTTAAAC ATTGGTTCCC TAGTCACCAT AGTTACCACT 2160  
 5 TGTATTTTAA GTCATTTTAA CAAGCCACGG TGGGGCTTTT TTCTCCTCAG TTGAGGAGA 2220  
 AAAATCTTGA TGTCACTACT CCTGAATTAT TACATTTTGG AGAATAAGAG GGCATTTTAT 2280  
 10 TTTATTAGTT ACTAATTCAA GCTGTGACTA TTGTATATCT TTCCAAGAGT TGAAATGCTG 2340  
 GCTTCAGAAT CATACCAGAT TGTCACTGAA GCTGATGCCT AGGAACTTTT AAAGGGATCC 2400  
 TTTCAAAAGG ATCACTTAGC AAACACATGT TGACTTTTAA CTGATGTATG AATATTAATA 2460  
 15 CTCTAAAAAT AGAAAGACCA GTAATATATA AGTCACCTTA CAGTCCTACT TCACACTTAA 2520  
 AAGTGCATGG TATTTTTCAT GGTATTTTGC ATGCAGCCAG TTAACCTCTG TAGATAGAGA 2580  
 20 AGTCAGGTGA TAGATGATAT TAAAAATTAG CAAACAAAAG TGACTTGCTC AGGGTCATGC 2640  
 AGCTGGGTGA TGATAGAAGA GTGGGCTTTA ACTGGCAGGC CTGTATGTTT ACAGACTACC 2700  
 ATACTGTAAA TATGAGCTTT ATGGTGTCTAT TCTCAGAAAC TTATACATTT CTGCTCTCCT 2760  
 25 TTCTCCTAAG TTTCATCCAG ATGAATATAA GCTAATATAC TATTATATAA TTCATTTGTG 2820  
 ATATCCACAA TAATATGACT GGCAAGAATT GGTGGAAATT TGTAATTAAA ATAATTATTA 2880  
 30 AACCTAAAAA AAAAAAAAAA AAAAATCTCGA G 2911

35 (2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

45 GGCACGAGCC CCAGGCCAGC CAGGGCCAGG CCTACTTTGG CCACCCTTAA ATTAGAATGT 60  
 GGGGTCAGGG GTCACAGAAA AGCCATTTCT CTGACCTAGT GTTTGGCGTC CGGGAACCTCT 120  
 GTGCCCAACC TTCAGACCCT GGCAGTCCTC ACTGAGGCCA TTGGCCCGAG GCCCGCCATC 180  
 50 CCCCAGARACC CCGGGGAGCC GCCTGTTGCC ACGTCCACAC CTGCCACACC CTCTGCCGGG 240  
 CCCCAGCCCC TCCCAACCGG GACCGTGCTG GTCCCTGGGG GTCTGCCCCC ACCTTGCCCTT 300  
 55 GGGGAGGCAT GGGCCCTCCT COTCCACCCC TGCCGGCGGT CACTCACCTC TTGCTTCTGG 360  
 TCCCCAGGC CTAGCCCTTG GAAGGAGACA GGAGTCTAGG GAGGCTGAAG CCCACTCCCC 420  
 60 GGGAGGCCCC TGCTCCTCCA GCCCCAGGGA CAGCAAGSAA AAGAGAAGAG AGCAGAGCAT 480

TTCATGGCTC TAATAAAAAA AAAAAAAAAA AAAACTCGA

519

5

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 968 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

15

TCCCTTGGG GCCGAAAAA GCGGGGTTGG CCTGNCCATT GGTNTCCAT GCGCCCGCC 60

CATGCCCCAG TACTAGCCTG CAGTCCCAAT GTAGCCCTC CCTCTCCMA GAGCCCTCM 120

20

AACC GCCCG STCANTTGTG ATTT CAGGAG GATTTGATGA AGATGTTAA GCGAAAGTGG 180

AGAACCTTCT CCGGATTTCC AGCCTGGAAA AAACGGACCC TGTTAGGCAA GCACCCTGCA 240

25

GCCCTCCCTG TCCCTTCTT CCCCTCCCCT TCYCCGCCC GTGGAGACAG CTGTTTTCAG 300

CAGGGCTCTC CGCAGGGAGG GGGCCGGCTC CTTCCCTGGC AGCAACATCC TTGCCCTTGT 360

CACACAAGTC AGCCTCCATC TGCGCAGCTC TGTGGATGCG CTGCTGGAGG GCAACAGGTA 420

30

TGTCACTGGC TGGTTCAGCC CCTACCACCG CCAGCGGAAG CTCATCCACC CGGTCATGGT 480

TCAGCACATC CAGCCGCGAG CGCTCAGCCT CCTGGCACAG TGGAGCACCC TCCTGCAGGA 540

35

GCTGGAGGCT GCCCTGCAGC TGGCTTTCTA CCCGGATGCC GTGGAGGAGT GCCTGGAGGA 600

AAACGTGCAC CCCAGCCTGC AGCGGCTGCA ARCTCTGCTG CAGGACCTCA GCGACGTGTC 660

TGCCCCCCCC CTGCCACCCA CCAGCCCTGG CAGGGACCTT GCTCAGGACC CCGAGGGGA 720

40

GAGCTCATGC CAGGGGGCTC CTGCTGGAGG CTGGGGGGGC TCTGCWYTRY CWWWTGCCCT 780

GGGCAATACG GCCCAGCTGG GCGTCGTGCC CTCTGGCCCA GCAGTGTCTT GCCCACACTC 840

45

AGTTCTGAG GCGCCTGGG AGCCCTGGG GCAGAGACTA GAAAACACAG AAGGAAGCAG 900

CACAGGGAGA CCGCTTTGT GATCTGCATG TGTGACACTG ATTCTTTGGA AATAAAGACT 960

GGAAGCTG 968

50

(2) INFORMATION FOR SEQ ID NO: 182:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

TGTAAGAGTT ATCAGTAATC CTAATTCCTT TCCTGGGTTT TCCTTTTGTC ACTTATTAAT 60  
 5 CAGTTTTTGA AAGGACGAAT GAATTTAGAG ATGTAATCTG GAGCACTATC ATGTTAAACC 120  
 ACGGGTATAT TAGAAAAATC ATCCTCATAA TCATTCTGGG AAGTTTTTCC TCCCCAAAAA 130  
 AAGCCATCCT GATGGGTTTT CAAAACCAGA AAAAAGCTCT TAATGAGGAA CAGACCACTG 240  
 10 GAGTACCCAT GAGCATCTCA GGAAGACTGA GACCCTCGAG AAGCCTTGAT TTCGTGCAAC 300  
 CCCCAGGTT TCAGAGCCAG CAGCCCACTG CTGTGGTTGA CAGACGTGGT TTTKTGGGA 360  
 15 AAGCAGCCAG AGGCCAGGAA TTTTCAGAGT CCGAGTCAC GRTVCCAC CCAAGATTAG 420  
 AGCAGAGATT AGCCATACTG AGATTGGTA AAATCATTCT GTCTAAGCA TGGAGGTGTG 480  
 TGCAGACGTG CAGTGCCTGT TCACAGGGGA TGCAGGCAGA TCS/GGGTTT AGGATGGGR 540  
 20 AGGCCACCGC ACCCCCYTTC AYTGCTCTGC ACCTGCTCCC TCACGTGGAC ACTGTCCACA 600  
 ACTGTGGCTC TCACAGGACA GTTCCCAAG GAGCTCATAT CTTATTGGAG ATAGGGGGTC 660  
 25 GTACAGGTGA CATTCACTAG CAGTGTGAGC CGGGTGACAT GGGGGTGTCA ACCCAGCATC 720  
 TGTCCAGGAG CTCCTCCTGC AGCGGCTCTG GCAGGTGGCC TGAGGCTCCT TTTTGAGAGA 780  
 GAACTGTTTG GCCTTCCTGT CTCCTCCTCT CTGATCTGTT CTTCTTTGGA ACACCACCA 840  
 30 AGAACCTCAC CTCCTCCATC AGATTGTGAG CTCCTGGAGG GCAGGAGCTG TGTCTTCTA 900  
 TTCATCTTCC TATCCCCAGA ACCTTGACA GATCCTGGAA TGTGGTAGGT GCTCAGTAAA 960  
 35 TGTGTGTGA ATAAATGAAT GAATGAATGA ACAAATGAAT GAATTTGCTT ACTTCAAGGC 1020  
 AAAAGAACCA TGAAGCTGA TTTGAGTTT CTATGTTATA GCAGTCAGCA AATCCTATTA 1080  
 40 AATACCTTGT GTTCCACGC AAAAAAAAAA AAAAAAAAAA AACTCGA 1128

## (2) INFORMATION FOR SEQ ID NO: 133:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CCGCGGCGTC TGACCTCATG GCGTAGAGCC TAGCAACAGC GCAGGCTCCC AGCCGAGTCC 60  
 55 GTTATGGCCG CTGCCGTCCC GAAGAGGATG AGGGGGCCAG CACAAGCGAA ACTGCTGCCC 120  
 GGGTCGGCCA TCCAAGCCCT TGTGGGTTG GCGGGCCCGC TGTCTTGGC GCTCCTGCTT 180  
 60 GTGTCCGCGC CTCTATCCAG TGTGTATCA CGGACTGAT CACCGAGCCC AACCGTACTC 240



	AACTCACATA TTTCTACCCC AAATGTGAAT GCTTTAACAC ATGAAAACCA AACCAAACCT	300
5	TCTATTTCCC AAATCAGCAC CACCCCTCCCT CCCACGACGA GTACCAAGAA AAGTGGAGGA	360
	GCATCTGTGG TCCCTCATCC CTCGCCTACT CCTCTGTCTC AAGAGGAAGC TGATAACAAT	420
	GAAGATCCTA GTATAGAGGA GGAGGATCTT CTCATGCTGA ACAGTTCTCC ATCCACAGCC	480
10	AAAGACACTC TAGACAATGG CGATTATGGA GAACCAAGCT ATGACTGGAC CACGGGCCCC	540
	AGGGACGACC ACGAGTCTGA TGACACCTTG GAAGAAACA GGGGTTACAT GGAAATTGAA	600
15	CAGTCAGTGA AATCTTTTAA GATGCCATCC TCAATATAG AAGAGGAAGA CAGCCATTTC	660
	TTTTTTCATC TTATTATTTT TGCTTTTTCG ATTGCTGTTG TTTACATTAC ATATCACAAC	720
	AAAAGGAAGA TTTTCTTCT GGTTCAAAGC AGGAAATGGC GTGATGGCCT TTGTTCCAAA	780
20	ACAGTGGAAAT ACCATCGCCT AGATCAGAAT GTTAATGAGG CAATGCCCTTC TTTGAAGATT	840
	ACCAATGATT ATATTTTTTA AAGCACTGTG ATTTGAATTT GOTTATGTAA TTTTATTTCG	900
25	TTGACTTTTT ATATGATATT GTCCAAATGT TTGCCATAGG CAATTGGTAC TTAATGAGA	960
	GGTGAGTCTC TCTTTTGCTT TGGTGCTTTG GAAATTAAT GTCACAAACG AGTATATAAT	1020
	TTTTIATCTG TACTTTTAGA GCTGAGTTTA ATCAGGTGTC CAAATGTGA GTTAAACATT	1080
30	ACCTTATATT TACACTGTTA GTTTTTATTG TTTTAGATTT ATTATGCTTC TTCTGGAAGT	1140
	ATTAGTGATG CTACTTTTAA AAGATCCCAA ACTTGTAAGT AAATTCGTAC ATATCTGTTA	1200
35	CTGCTGACTC ACATTCATTC TCCGCCATTC AAATACTATT TTTTATCCAC ATTTTTTTTT	1260
	GTTCCCAAAC TGTAATGTAC AAGGATATGT GTGATAATCC TTGGGATTTC ACTAATATTT	1320
	TTTTTCTTC CAAGAAACT GCTTTGGATA TTTTAGATA ATTTAAACAT AATTTAGGAT	1380
40	AATGATATTG CTCAATCTGA CCACAATTTT AGGTAAAACA TTAAATGTGT CAGAAATCTT	1440
	GGCAACAGAG ACTCTGCAGC TTGCAGTGGG CATAGATAAA ATGTTACAGA GATACTATTT	1500
45	TTTTGGTTGG AATTACTATA TTAAATTTAG AAGCAGAAAC TGGTAAATG TTAAATACAT	1560
	GTACAATTGC TTTTAGTTAG CAATTGATTG TAGCATGGGT TCCTCCAAGG TTTCAAGCAA	1620
	TGGGCAGAGT TTAATTTAT ATCAGATTGG TTTACTTGGT TTATTATTTT ACAGTAAATT	1680
50	TGAATAAATC TTAGGGGTCA TTATCACTTA AATAACTATG TACCTAGGTC TTTCAAATTA	1740
	AAATTATACC TGAATGAAGT TGTTTGATA CATAAAGGAT ATTTGTGTAC AATTACCTTT	1800
55	TTTCCCCCAC ACTTGTTTTT TTTGTTTTTG TTTTATGG CAACTGGAAA GTATTTACTA	1860
	TGGGATTCAT TTATGTCGT CTTTCTATCA TAAAGAATTG ATCAATATGT AAATATGTGA	1920
	TTTGAACCAT GGTGACTTA CAAGTGTCAC TACAGCTTTT TAGAAAACAT AGCCCTAATA	1980
60	TATGTTAAGC AGGACCCGGG TGAGCCAGTG GGCTTGCGCT TTATGTAGAG CTGGAGAGG	2040

GCGCTCCATC CTGTCTCTTG GCGGACAGT GTACTTTCCT AATAGGGAAG GGAAGCACAA 2100  
 TGGAAATACC CCTGAACCGT TTTATTGCAG TAATTTTTTT CATATCTGAA ACTATTATTT 2160  
 5 AATATTTTGA ATAAGATTTT AAAAAATAAA TGCCAAAGAT ATAAATCTAA AAAAAAAAAA 2220  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2276

10

(2) INFORMATION FOR SEQ ID NO: 184:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TCCAAGCTAC GCCACTCGGG CTGGGGCGTT GGGAGCGGGA GTGCAGAGCG TGGTCGTGGC 60  
 25 GCGCGCGGTG AGAAGAGCGA GGCGKAGGAG GGGGTGCCAT GCGCGGGCAG CAGTTCAGT 120  
 ACGATGACAG TGGGAACACC TTCTTCTACT TCCTCACCTC CTTCGTGGGG CTCATCGTGA 180  
 TCCCGCGCAC ATACTACCTC TGGCCCCGAG ATCAGAATGC CGAGCAAAAT CGATTAAAGA 240  
 30 ATATCAGAAA AGTATATGGA AGGTGTATGT GGTACGTTTA CGGTTATTAA AACCCAGCC 300  
 AAATATTATT CCTACAGTAA AGAAAATAGT TCTGCTTGCA GGATGGGCAT TGTCTTATT 360  
 35 CCTTGCATAT AAAGTTTCCA AACAGACCG AGAATACCAA GAATACAATC CTTATGAAGT 420  
 ATTAATTTTG GATCCTGGAG CCAAGTAGC AGAAATTAAA AAACAATATC GTTGTCTGTC 480  
 ACTTAAATAT CATCCAGATA AAGGAGGTGA TGAGGTTATG TTCATGAGGA TAGCAAAAGC 540  
 40 TTATGCTGCT TTAACGGATG AAGAGTCCCG GAAAAATTGG GAAGAATTTG GAAATCCAGA 600  
 TGGGCTCAA GCCACAAGCT TTGGAATTGC CCGCCAGCT TGGATAGTTG ACCAGAAAAA 660  
 45 TTCAATTCTG GTTTTACTTG TATATGGATT GGCATTTATG GTTATCCTTC CAGTGTGTGT 720  
 GGGCTCTTGG TGGTATCGCT CAATACGCTA TAGTGGAGAC CAGATTCTAA TACGSACAAC 780  
 ACAGATTIAT ACATACTTTG TTTATAAAAC CCGAAATATG GATATGAAAC GTCTTATCAT 840  
 50 GGTTTTGGST GGAGCTTCTG AATTGATCC TCAGTATAAT AAAGATGCCA CAAGCAGACC 900  
 AACGGATAAT ATTCTAATAC CACAGCTAAT CAGAGAAAT GGCAGCATTA ATTTAAAGAA 960  
 55 GAATGAGCCT CCACTTACCT GCCCATATAG CCTGAAGGCC AGAGTTCCTT TACTGTCTCA 1020  
 TCTTGCTAGA ATGAAAATTC CTGAGACCCT TGAAGAAGAT CAGCAATTCA TGCTAAAAAA 1080  
 GTGTCTGCC CTACTTCAAG AATGGTTAA TGTAATCTGC CAACTAATAG TAATGCCCCG 1140  
 60

GAACCGTGAA GAAAGGGAGT TTCGTGCTCC AACTTTGGCA TCCCTAGAAA ACTGCATGAA 1200  
 GCTTTCTCAG ATGGCCGTTT ACGGACTTCA GCAATTTAAG TCTCCCTTC TGCAGCTCCC 1260  
 5 TCATATTGAA GAGGACATC TTAGACGGGT TTCTAATCMT AAGAAGTATA AAATTPAAAC 1320  
 TATCCAGGAT TTGGTGAGTT TAAAAGAATC AGATCGTCAC ACTCTACTGC ACTTCCTTGA 1380  
 10 AGATGAAAAA TATGAAGAGG TTATGGCTGT CCTTGGGAGT TTTCCATATG TGACCATGCA 1440  
 TATAAAATCA CAGGTGTTAG ATGATGAAGA TAGCAACAAC ATCAGAGTAG GATCCTTAGT 1500  
 TACAGTGTG GTTAAGTTGA CAAGGCAAC AATGGCTGAA GTATTTGAAA AGGAGCAGTC 1560  
 15 CATCTGTGCT GCAGAGCAAC AGCCAGCAGA AGATGGGCAG GGTGAAACTA ACAAGAACAG 1620  
 GACAAAAGGA GGATGCCAAC ACAAGAGTAA AGGACCCAAG AAAACTGCTA AATCAAAAAA 1680  
 AAAGAAACCT TTAACAAAAA AACCTACACC TGTGCTATTA CCACAGTCBA AGCAACAGAA 1740  
 20 ACAAAGCAG CCAATGCGAG TCGTTGGGAA TGAAGCTGCA GTAAAGGAAG ATGAAGAAGA 1800  
 AGTTTCAGAT AAGGGCAGTG ATTCTGAAGA AGAAGAAACC AATAGAGATT CCCAAAGTGA 1860  
 25 GAAAGATGAT GGTAGTGACA GAGACTCTGA TAGAGAGCAA GATGAAAAAC AAAACAAAGA 1920  
 TGATGAAGCA GAGTGGCAAG AATTACAACA AAGCATACAG CGAAAAGAGA GAGCTCTATT 1980  
 GGAAACCAA TCAAAAATAA CACATCCTGT GTATAGCCTT TACTTTCCCTG AGGAAAAACA 2040  
 30 AGAATGGTGG TGGCTTTACA TTGCAGATAG GAAGGAGCAG ACATTAATAT CCATGCCATA 2100  
 TCATGTGTGT ACGCTGAAAG ATACAGAGGA GGTAGAGCTG AAGTTTCCTG CACCAGGCAA 2160  
 35 GCCTGGAAAT TATCAGTATA CTGTGTTTCT GAGATCAGAC TCCTATATGG GTTTGGATCA 2220  
 GATTAACCA TTGGAAGTTK CGAAGTTTAT GAGGCTGAAG CCTGTGCCAG AAAATCACCC 2280  
 ACAGTGGGAT ACAGCAATAG AGGGGGATGA AGACCAGGAG GACAGTGAGG GCTTTGAAGA 2340  
 40 TAGCTTTGAG GGAGGAAGAG CGAGGGAGGA AGGAAGGTGG TGGACTTAAG GCAGTTACTC 2400  
 TGAATGGGA CCCACAGTGT TTTGCACCAT ATTTTGGCAA TTTTTCCTGC CCGTTTTTNG 2460  
 45 GAAGTGTITT CONTNAANCC CAGGAACCAT TACAGAACCG 2500

50 (2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1337 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

60 CTTCCCGTTT TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CSACCGGGCC

80

5  
10  
15  
20  
25  
30  
35  
40  
45

TCTCCCTGGC GTTGGTGCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGA 120  
GCCAGCGTGG CGGGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG 180  
GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCCTCT CCTGCTGTTG 240  
CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT 300  
CTTGGGCCTC CTGACCCTAG ACCACGGACA TTACCGCCGC TGCCACCGGG CCTTACCCCT 360  
GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGG CGCGGGGCTC CGAGGGAGGC 420  
AATGGCAGCA ACCCTGTGGC CGGGCTTGAG ACGGACGATC ACGGAGGGAA GCGCGGGCAA 480  
GGCTCGGTGG GTGCGGGCCT TGCTGTGAGC CCCAACCCTG GCGACAAGCC CATGACCCAG 540  
CGGGCCCTGA CCGTGTGAT GGTGCTGAGC GCGCGCGTGC TGGTGTACTT CCGGTGCAGG 600  
ACGGTCAGGA TGAGAAGAAG AAACCGAAAG ACTAGGAGAT ATGGACTTTT GGACACTAAC 660  
ATAGAAAATA TGGAATTGAC ACCTTTAGAA CAGGATGATG AGGATGATGA CAACACGTTG 720  
TTTGATGCCA ATCATCCTCG AAGATAAGAA TGTGCCTTTT GATGAAAGAA CTTTATCTTT 780  
CTACAATGAA GAGTGAATT TCTATGTTTA AGGAATAAGA AGCCACTATA TCAATGTTGG 840  
GGGGGTATTT AAGTTACATA TATTTTAACA ACCTTTAATT TGCTGTTGCA ATAAATACCG 900  
TATCCTTTTA TTATATCTTT ATATGTATAG AAGTACTCTR TTAATGGGCT CAGAGATGTT 960  
GGGGATAAAG TATCTGTAA TAATTTATCT GTTTGAAAAT TACTATAAAA CCGTGTTTTC 1020  
TGATCGGTTT TTGTTTCCTG CTTACCATAI GATGTAAAT TGTTTTATGT ATTAATCAGT 1080  
TAATGCTAAT TATTTTGTCT GATGTCATAT GTTAAAGAGC TATAAATTCC AACACCAAC 1140  
TGGTGTGTAA AAATAATTTA AAATTTCTT TACTGAAAGG TATTTCCCAT TTTTGTGGG 1200  
AAAAGAAGCC AAATTTATTA CTTGTGTG GGGTTTTTAA AATATTAAGA AATGTCTAAG 1260  
TTATTGTTTG CAAAACAATA AATATGATTT TAAATCTCT TAAAAA AAAA AAACC 1320  
CCCGGGGGGG GCGCGN 1337

50 (2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 941 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

60 GGCACGAGCC TGGACGCAGC AGCCACCGCC GCGTCCCTCT CTCACGAGG CTGCGCGCTT 60

AGGACCCCCA GGTCCGACAT GTCCGCTCTT GGTCCGCTGT GTCTTCTCAG CATCGTTGGC 120  
 CTGATTCTCC CCACCAGAGG ACAGACGTTG AAAGATACCA CGTCCAGTTC TTCAGCAGAC 180  
 5 TCAACTATCA TGGACATTCA GGTCCCGACA CGAGCCCGAG ATGCAGTCTA CACAGAACTC 240  
 CAGCCCACTT CTCCAACCCC AACCTGGCCT GCTGATGAAA CACCACAACC CCAGACCCAG 300  
 10 ACCCAGCAAC TGGAAAGAAC GGATGGGCCT CTAGTGACAG ATCCAGAGAC ACACAAGAGC 360  
 ACCAAAGCAG CTCATCCCTC TGATGACACC ACGACGCTCT CTGAGAGACC ATCCCAAGC 420  
 ACAGACGTCC AGACAGACCC CCAGACCTTC AAGCCATCTG GTTTTCATGA GATGACCCC 480  
 15 TTCTTCTATG ATGAACACAC CCTCCGGAAA CCGGGGCTGT TGGTCGCAGC TGTGCTGTTT 540  
 ATCACAGGCA TCATCATCCT CACCACTGCC AAGTGCAGGC AGCTGTCCCG GTTATGCCGG 600  
 AATCATTTGCA GGTGAGTCCA TCAGAAACAG GAGCTGACAA CCGCTGGGGC ACCCGAAGAC 660  
 20 CAAGCCCCCT GCCAGCTCAC CGTGCCGAGC CTCCTGCATC CCCTCGAAGA GCCTGGCCAG 720  
 AGAGGGAAGA CACACATGAT GAAGCTGGAG CCAGGGCTGC CCGTCCGAGT CTCCTACCTC 780  
 25 CCCCACCCCT GCGCGCCCTT GAAGGCTACC TGGCGCCTTG GGGGCTGTCC CTCAGTTAT 840  
 CTCCTCTGT/ AAGACAAAAA GTAAAGCACT GTGGTCTTTT CAAAAAATAA AAAAAAATAA 900  
 AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAACTCG A 941  
 30

## (2) INFORMATION FOR SEQ ID NO: 187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GAATTCGGCA CGAGGCAGCT TGTGCTTTAA AGGAGGTGTT CAAAGCATGT CTGAGCAGAG 60  
 45 ACTTTTGGGC TCTGTTTTAA TTAATACTTT AAAATAATTC ATATTTAAAA TATCATATGT 120  
 TTCCATAAAG AGGAGGATGT TTAATGCCT CCAGACTACA TTCTTTTATA TTCTTTGATT 180  
 50 TTACCTGGGA GTCCAAAGTT CAATTCCCAT AAAGCAAGCG TTTTATTTGT CACTTTCAAT 240  
 ATACATCCGA TTGCCATGCT TAAGATGCAA TATGGGCTGC GGAAATAGGT TAACCCACAG 300  
 GCTCCCAAGG CCCAGTGTAG AAGGTGAGAG ATTGCTGTAA AATGATTCAA ATAAAGGAA 360  
 55 GACCTGGGC GGCTGCCGTA RCTCAGCCT GTAATCCGAG CACTTTGGGA GGCCGAAGCG 420  
 AGTGGATGAC GAGGTTAGGA GTTGAGACC AGCCTGGCCA ACATCGTGAA ACCCCGTCTC 480  
 60 TACTAAAAAT ACAAATAA GCGGGCATG GTGGCAGCA CCTGTAATCC TAGCTAGTTG 540

GGAGGCTGAG GCAGGAGAAT CGTTTGAATC TGGGACTTGG AGGTTGTCAG TCAGCTGAGA 600  
 TCGCGCCACA GCACTCCAGC CTGGGTGACA GGGTGAGACT CTGTCTCAAA NAGA 654

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1848 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GAAACTGGAC CGGAGAACCG GAGCGAAGCG AAGCGGAAGC CCGGAATGAG CCGGACTGG 60  
 AAAGCCGGAG CGGGGCCAGG CGGGCCTCCC CAAAAGCCTG CCCCTTCATC CCAGCCGAAA 120  
 CCGCCGGCCC GCGCGAGCGC GCGGGCCCGT GCGATTGCAG TCGCGGGCGC GGAGGAAGAG 180  
 25 AGACGGCTCC GGCAGCGGAA CCGCCTGAGG CTGGAGGAGG ACAAACCGGC CGTGGAGCGG 240  
 TGCTTGGAGG AGCTGCTCTT CCGCGACGTC GAGAACCAGC AGGACCGCTT GCTGCGGCGT 300  
 CTGCGAGGCC CGAGGGTTCA AGAACATGAA GACTCGGGTG ACTCAGAAAT GGAGAATGAA 360  
 30 GCAAAAGGTA ATTTTCCACC TCAAAAGAAG CCAGTTTGGG TGGATGAAGA ACATGAAGAT 420  
 GAGGAAATGG TTGACATGAT GAACAATCGG TTTCGGAAGG ATATGATGAA AAATGCTAGT 480  
 35 GAAAGTAAAC TTTCGAAAGA CAACCTTAAA AAGAGACTTA AAGAAGATT CCAACATGCC 540  
 ATGGGAGGAG TACCTGCCTG GGCAGAGACT ACTAAGCGGA AAACATCTTC AGATGATGAA 600  
 AGTGAAGAGG ATGAAGATGA TTGTTGCAA AGGACTGGGA ATTTTCATATC CACATCAACT 660  
 40 TCTCTTCCAA GAGGCATCTT GAAGATGAAG AACTGCCAGC ATGCGAATGC TGAACGTCCT 720  
 ACTGTTGCTC GGATCTCCAT CTGTGCAGTT CCATCCCGGT GCACAGATTG TGATGGTTGC 780  
 45 TGGGATTAGA TAATGCTGTA TCACTATTTT AGGTTGATGG GAAAACAAAT CCTAAAATTC 840  
 AGAGCATCTA TTTCGAAAGG TTTCGAATCT TTAAGGCTTG TTTTAGTGCT AATGGGGAAG 900  
 AAGTTTTAGC CACGAGTACC CACAGCAAGG TTCTTTATGT CTATGACATG CTGGCTGGAA 960  
 50 AGTTAATTCC TGTGCATCAA GTGAGAGGTT TGAAGAGAA GATAGTGAGG AGCTTTGAAG 1020  
 TCTCCCAGA TGGTCTTTC TTGTCATAA ATGGCATTGC TGGATATTTG CATTTGCTAG 1080  
 55 CAATGAAGAC CAAAGAAGTG ATTGGAAGCA TGAATAATTA TGAAGGGTT GCAGCATCCA 1140  
 CATCTCTTTC AGATAGTAAG AAAGTATACG CCTCTTCGGG GCATGGAGAA GTTTATGTTT 1200  
 60 GGGATGTGAA CTCAAGGAAG TGCCTTAACA GATTGTGTTA TGAAGGCAGT TTATATGGAT 1260

TAAGCATTGC CACATCTAGG AATCGACAGT ATGTTGCTTG TGGTCTAAT TCTGGAGTGG 1320  
 TAAATATATA CAATCAAGAT TCTTGTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA 1380  
 5 TAATGAACTT GGTACAGGT GTTACTTCTC TGACCTTCAA TCCTACTACA GAATCTTGG 1440  
 CAATTGCTTC AGAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG 1500  
 10 TATTTTCAA CTTCCAGTC ATTAAAATA AGAATATTTT TCATGTTTAT ACCATGGATT 1560  
 TTTCTCCGAG AAGTGGATAC TTTGCCTTGG GGAATGAAA GGGCAAGGCC CTGATGTATA 1620  
 GGTGCAACCA TTAATCAGAG TTCTAAAGAG ACTATTTGAA GTCCAGTTGA GTCACAAGAG 1680  
 15 AAGCCTGTCT TGATATATCA TCTCAGAAAC TTTCTGAAT ATGTGATAAT ATATGAAAA 1740  
 TGATTTATAG ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAAACA TGTGGCAGCT 1800  
 20 TTTGTTTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACTCGA 1843

## (2) INFORMATION FOR SEQ ID NO: 189:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AAAAAAACC CAGGGGAACN TTGGGGGCCG CTTTNNMTTC CCCCTCCAGG CCATTGGGGA 60  
 35 ATTCTTCAAG TTAATCTGCT TTTGCTCTTG GCCAACAGGG CTTGTAGGGG GGAGAGACCC 120  
 AGGATCATCA AGGGGTTCCA GTGCAAGCCT CACTCCAGC CTTGGCAGGC AGCCCTGTTC 180  
 40 GAGAAGACGC GGCTACTCTG TGGGGCGACG CTCATCGCCC CCAGATGGCT CCTGACAGCA 240  
 GCCCCTGCCC TCAAGCCCCG CTACATAGTT CACCTGGGGC AGCACAACCT CCAGAAGGAG 300  
 GAGGCTCTG AGCAGACCCG GACAGCCACT GAGTCTTCC CCCACCCCGG CTTCAACAAC 360  
 45 AGCCTCCCCA ACAAGACCA CCGCAATGAC ATCATGCTGG TGAAGATGGC ATCGCCAGTC 420  
 TCCATCAGCT GGGCTGTGGG ACCCCTCACC CTCTCTCAC GCTGTGTCAC TGCTGGCACC 480  
 50 AGCTG/CTCA TTTCCGGCTG GGGCAGMACG TCCAGCCCCC AGTTACGGCT GCCTCACACC 540  
 TTGSGATGCG CCAACATCAC CATCATGAG CACCAGAAGT GTGAGAAGCG CTACCCCGGC 600  
 AACATCACAG ACACCATGGT GTGTGCCAGC GTGCAGGAAG GGGGCAAGGA CTCCTGCCAG 660  
 55 GGTGACTCCG GGGGCCCTCT GTCTGTAAC CAGTCTCTTC AAGGCATTAT CTCCTGGGGC 720  
 CAGGATCCGT GTGCGATCAC CCGAAAGCCT GGTGTCTACA CGAAAGTCTG CAATATGTG 780  
 60 GACTGGATCC AGGAGACGAT GAAGAACAAT TAGACTGGAC CCACCCACCA CAGCCCATCA 840

CCTCCGATTT CCACTTGGTG TTGCTTCCT GTTCACTCTG TTAATAAGAA ACCCTAAGCC 900  
 AAGACCTCTT ACGAACATTC TTTGGGCTTC CTGGACTACA GGAGATGCTG TCACTTAATA 960  
 5 ATCAACCTGG GGTTCGAAAT CAGTCAGACC TGGATTCAAA TTCTGCCTTG AAATATTGTG 1020  
 ACTCTGGGAA TGACAACACC TGGTTTGTTC TCTGTTGTAT CCCCAGCCCC AAAGACAGCT 1080  
 10 CCTGGCCATA TATCAAGGTT TCAATAAATA TTTGCTAAAT GAAAAAATAA AAAAAAAAAA 1140  
 ACTCGA 1146

15

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 906 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ACTCCCTCAC CCAGGTCCCA GCCCTGGGAA'CCACCTACCG TGAGCCCTTT TGCAGATATA 60  
 GACTCATTTC ATCCTCAGAT GGTCTTCAA GGTAGGTACT TTAGTCCCAT TTTAGAGATG 120  
 30 AGACCATTGA GGCAGAGGG GTGNGTAAC TTGCCTGGG GCTCAGGAGC ACAAAGGAG 180  
 CCGAGGCAGG ATCTGACCCT TGTTCTCTGG CCTCACTGCC CTCACTTTGC CATGACCCGA 240  
 35 AGTTATGTCC CTACAAAGCA ATGCATGGTC CAAGGYTCTT TTTATTGTAT TTTTATTTT 300  
 AAGGTCCTG TTCAAACTG GTGTGAGCTC TGAGGAGTCC TGAACCCTGG GTGCAGCATC 360  
 CTAGCATCCT GGGAGTCTT TTCTGCCAC ACTGAGCTGG GTCCTCGAG GGTGGGGCT 420  
 40 GCTGTCCCTG GAAGCCTGGC AGCAGCACTG TATCGGGTTG GCTGAAGCTG ARCSCCGTGG 480  
 GGTGCAGGGC TCCMGAATC CCGTTTGGC TGAAGGGGT CCGTGTAGCC MGGGATGTTT 540  
 45 ATGAGGTCTC TCTGATGCCC CAGGCCGAGC ACATGTGTCC GGTGGAGAA AAGCAGGCCC 600  
 TTTCACTGCC AGCTCCACTC AATTTCTATG TGGACCAAGA ACGATAAACT TAAAAAATT 660  
 TTTTCTCTAA GGTATCTTCA GAATATGGTG TATTTTATG TGGAAAAGAA AAGTTATGAA 720  
 50 GGCAGCTGTT ACTTTAAGAG AAAATTCATT AAAAGTCCTC GAGGTATGAA GATGACGGCG 780  
 TGCTTCTCAA TCATTTTGGC ATAAGTTGAT TGTGGCTGTA ATTTTTTTTT TTTTPTTGT 840  
 55 CAAGCATGTC AGACAATAAA GTCTTTGTAA AAAGRGAAAA AAAAAAAAAA AAAAAAAAAA 900  
 ACTCGA 906

60



## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1941 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTTCAGCTGA AGCCAGGGA CCCCTTTTC ACCCTGGGC CCAATGCCGT CCTTTCGGC 60  
CAGAGACTGG TCTTGGAAAC CTCAGCAAA CTCAGCATCC AGGACAACAA TGTGGACCTG 120  
ATTCTGGCCA CACCCCCCTT CAGCCGCCTG GAGAAGTTGT ATAGCACTAT GGTGCGCTTC 180  
CTCAGTGACC GAAAGAACCC GGTGTGCCCG AGATGGCTGT GGTACTGCTG GCCAACCTGG 240  
CTCAGGGCGA CAGCCTGGCA GCTCGTGCCA TTGCAGTGCA GAAGGGCAGT ATCGGCAACC 300  
TCCTGGGCTT CCTAGAGGAC AGCCTTGCCG CCACACAGTT CCAGCAGAGC CAGGCCAGCC 360  
TCCTCCACAT GCAGAACCCA CCCTTTGACC CAAVTAGTGT GGACATGATG CGGCGGGCTG 420  
CCGCGCGGCT GCTTGCCCTG GCCAAGGTGG ACGAGAACCA CTCAGAGTTT ACTCTGTACG 480  
AATCACGGCT GTTGACATC TCGSTATCAC CGTTGATGAA CTCATGGTT TCACAAGTCA 540  
TTTGTGATGT ACTGTTTTTG NATTGGCCAG TCATGACAGC CGTGGGACAC CTCCCCCCCC 600  
CGTGTGTGTG TCGGTGTGTG GAGAACTTAG AAAGTGACTG TTGCCCTTTA TTTATGCAAA 660  
ACCACCTCAG AATCCAGTTT ACCCTGTGCT GTCCAGCTTC TCCCTTGGGA AAAAGTCTCT 720  
CCTGTTTCTC TCTCCTCCTT CCACCTCCCC TCCTCCATC ACCTCAGGC TTTCTGTTC 780  
TTGTCTCAC CTTACTCCCC TCAGGACCCT ACCCCACCCT CTTGAAAAG ACAAAGCTCT 840  
GCCTACATAG AAGACTTTTT TTATTTTAAC CAAAGTACT GTTGTTTACA GTGAGTTTGG 900  
GGAAAAA TAAATAAAA ATGGCTTTCC CAGTCCTTGC ATCAACGGGA TGCCACATTT 960  
CATRACTGTT TTATATGGTA AAAAAAATA AAAAAAATAC AAAAAAAT TCTGAAGGAC 1020  
AAAAAAGGTG ACTGCTGAAC TGTGTGTGGT TTATTGTTGT ACATTCACAA TCTTGCAGGA 1080  
GCCAAGAAGT TCGCAGTTGT GAACAGACCC TGTTCACCTG AGAGGCCTGT GCAGTAGAGT 1140  
GTAGACCTTT TCATGTACTG TACTGTACAC CTGATACTGT AACATACTG TAATAATAAT 1200  
GTCTCACATG GAAACAGAAA ACGCTGGGTC AGCAGCAAGC TGTAGTTTTT AAAAATGTTT 1260  
TTAGTTAAAC GTTGAGGAGA AAAAAAATA AGGCTTTTCC CCCAAAGTAT CATGTGTGAA 1320  
CCTACAACAC COTGACCTCT TTCTCTCTC CTTGATTGTA TGAATAACCC TGAGATCACC 1380  
TCTTAGAACT GGTTTTAACC TTAGCTGCA CGNCTACGT CNAWCGNTGT GTATATATAT 1440  
GACGTGKTAC ATTGCACATA CCGTTGGATC CCCACAGTTK GGTCTCTCTC CCAGCTACCC 1500

CTTTATAGTA TGACCAGTTA ACAAGTTGGT GACCTGCACA AAGCGAGACA CAGCTATTTA 1560  
 ATCTCTTGCC CAGATATCGC CCTCTTGGT GCGATGCTGT ACAGGTCTCT GTAAAAAGTC 1620  
 5 CTTGCTGTCT CAGCAGCCAA TCAACTTATA GTTTATTTTT TTCTGGGTTT TTGTTTTGTT 1680  
 TTGTTTTCTT TCTAATCGAG GTGTGAAAAA GTTCTAGGTT CAGTTGAAGT TCTGATGAAG 1740  
 10 AAACACAATT GAGATTTTTT CAGTGATAAA ATCTGCATAT TTGTATTTCA ACAATGTAGC 1800  
 TAAAACTTGA TGTAATTCCT TCCTTTTTTT CCTTTTTTGG CTTAATGAAT ATCATTTAAT 1860  
 CAGTATGAAA TCTTTATACT ATATGTTCCA CGTGTTAAGA ATAAATCTAC ATTAATCTTT 1920  
 15 GGTAAAGACTT TAAAAAATAA A 1941

20

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2118 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

30 AATAATAAT AANAATRAAT AAAARTWAAG TGCTTARTGT AACTCAGCGG ACAGGGCTCC 60  
 CAGCTGCTCT GGCACGTGGG ACACCTTCCA CCTGTCACAC AACAGGCATG CAAAGAGGAC 120  
 35 TGGATATGGT GGGGTAGAGT GCTTCTGGTG TGTTCACTTT AAGAAAACAT CTGCCAAGAG 180  
 AGAAGAGTGC CCAGGAAGA CCAGGAAAT ACAAGTACAT GGCTGCTTCA TACCATATAC 240  
 CCCAATTCTT TAAAGCAGCA AAAGGCACTT TTTTTTTCAG GCCAGAGTGA ATCTAAAACA 300  
 40 AACCTGGCTT TGCTTACAGG GAAGCTGTCC CAGAAGGACT GAGTGATGCC TCTTGTCCCC 360  
 TAAGGTCTGG AGAGTCTTTG CAAGTTTCCA ACGACATTTC CACCAGGTG GGAGAGACCA 420  
 45 GCAGTTGACG AGACAAGTCA GACCCAAAAA ACGACGCCAA CGTAGTGAGT GCGTGCTTAT 480  
 TTGGGAGTAG GATGATTGA GAAAAACAGG AAGAAAAACC GGTGAGAAAG TGGCACTTTG 540  
 GAAGTGGAAG GCTGTTTCCA AATAGCAACT CTGGCTAAAG CGAAATGTT AATCAAGTAG 600  
 50 AAAGTAAAT TCAGGATCTT AGAAGCTCAT CCTTCTGATG AGAACTATTT TTTTTCCGT 660  
 GAAGGAACCT TTATTACTTT AAAAGTGAGG GTAATTTACA TATGGGTGT ATATATTCTA 720  
 55 AAAATAGTAA TAAAGTACC TTTTATAAGC AATGTTGTGT GGCTTGTTAG AGAAAGCAGG 780  
 GAGGAAAAAA AGGCAGGCAA AACTAGTCTA GGTCTAGGCC CTAAAAATGA GCTTCCTTCC 840  
 CACTTGACTG GAAACGCCCA TGTGATTCT AGGCTGAAAA TAGGTAGGAT TTAACGAGTA 900  
 60

	ACCTAGTTCC CTTCTGTCTC TGATTTCGA TCAGCTGATG GAGGTGCTAG TAAGAGGGGC	960
	CGATCATGCT CCGAGACGAG TCCTTTGGCC TCTTGCTCTC CATCCCAAGC CTGACTCCTT	1020
5	CAGCAGCAGC CCCCTCCTTC TGTGTCCATC TGATGCAGGC AAGCAGGAGC AGTAACAGGG	1080
	CATCCCATGT TCCAGTTCAC CTTCTATGGG GTGACTARGA GGTTCOCGGT AACTAGGGCA	1140
10	GCCCARGCCC AGCAGGTTCG AAAAGCAGCT GCAAGCTTCA GAAACCCACT TCCTCCAACA	1200
	CCAGGGAGGT GGCAGAGAGC CCATCCAAAA GCCCACTGGG AGAGGCATAA GATTCTGTGC	1260
	CAGGCCCCCA GCTCCCTCTC GTGTGAGTA GGCTGTGCTA CTGGCCTCTG AAGTAAAGGC	1320
15	AAANACAAAC GCGCAGGCCA GGGTGGCAGG AATAAAAAAC TCTGGACAGA AACCCTTTTA	1380
	ATAAAGGAAA TTCCACCCCT CCCAATCCTT CCATGGAAGG GTGAGACCTT ANTGTGATGT	1440
	AAGAGGAAGG TCTTCTCTGG CTTTCAGGGA AACAGCTGCA GCTGAAACTT AGGGGCCCAT	1500
20	TCCAGGGCAC TTTTCACCAC AGCCAGTGCA GCCGCTCCAA GTGCCACTGT CAGCCCCATC	1560
	ACTGCCAATT TCACAAAGCG GTTGGTCCTT GGCTTGGTCA GCACATCTTT TGTTCGATCT	1620
25	TCAGGGCCCA GAAGTCCCCG AANACCCCTG CCGCAGCACC ATATCAGGCC TCTGCTGGGC	1680
	TGATGCCAGC TCAAAGTCTT TGAAGTAGA GGCTGCCGTC CTCTCAGCTT GCTGTGGGC	1740
	AGCGGCCTCC CGAGCAAGTT CGGATGGGGG AACTGAACA AAAAGGTCTC CTSTCTGCTG	1800
30	ATCAGTGTCT CATAGGCCAA GTCTGAGGG ATCTGGGACA ACAGGTGGTG GACCGAGGCC	1860
	ATGTACAGT CACAGTCCAG GACTTCCTGC TCGCGATACA ACACAATCAC GGCTGCAAAG	1920
35	TAAATCGGCA TCAGTGGGTG GCAGGCCAGG AAGAAGTCAT ATAACCGCAC GACGTGCCTG	1980
	AAGTCAGACA GCACATGCCC AAACCAGGTG ATGAGCCAGC TGAGGGCAA GATGGTCCCT	2040
	ACCTCAGCAC TCTGCATGAA GTCATGGAGC TCTGGATTCA CTTGGTCAAT CATGGGCATC	2100
40	AGATAGTTTA ATATATGC	2113

45

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1538 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

55

	CCGGGTTGGG CTCTGTGTCA GCAGCCGGGC GCGGCTGGGG CGGGACATGG CAGCCTGTAC	60
	AGCCCCGGGG CCTGGCCGTG GGCAGCCGCT GGTGCTCCCG GTGCTGACT GNGGCCCGGT	120
60	GGCCAAGGCC GCTCTGTGGC CGGCCGNAGC TGGAGCCTTC TCGCCAGCGT CGACCACGAC	180

5 GACCGGGAGG CACCTCTCGT CCCGAAACCG ACCAGAGGGC AAAGTGTGAG AGACAGTTGG 240  
 TGTGTTTGAG GTGCCAAAAC AGAATGGAAA ATATGAGACC GGGCAGCTTT TCCTTCATAG 300  
 CATTTTTGGC TACCGAGGTG TCGTCTGTT TCCTGGCAG GCCAGACTGT RTGACCGGGA 360  
 TGTGGCTTCT GCAGCTCCAG AAAAAGCAGA GAACCTGCT GGCATGGCT CCAAGGAGGT 420  
 10 GAAAGGCAAA ACTCACACTT ACTATCAGGT GCTGATTGAT GCTCGTGA CTGACATAT 480  
 ATTCAGAGA TCTCAGACAG AAGCTGTGAC CTCTTGGCT AACCATGATG ACAGTCGGGC 540  
 CCTCTATGCC ATCCCAGGCT TGGACTATGT CAGCCATGAA GACATCCTCC CCTACACCTC 600  
 15 CACTGATCAG GTTCCCATCC AACATGAACT CTTTGAAAGA TTTCTTCTGT ATGACCAGAC 660  
 AAAAGCACCT CCTTTTGTGG CTCGGGAGAC GCTAAGGGCC TGGCAAGAGA AGAATCACCC 720  
 20 CTGGCTGGAG CTCTCCGATG TTGATCGGGA AACAACTGAG AACATACGTG TCACTGTGAT 780  
 CCCCTTCTAC ATGGCCATGA GGAAGCCCA GAATTCACAC GTGTACTGGT GGGCTACTG 840  
 TATCCGTTTG GAGAACCTTG ACAGTGATGT GGTACAGCTC CGGAGCGGC ACTGGAGGAT 900  
 25 ATTGAGTCTC TCTGGCACCT TGGAGACAGT GCGAGCCCGA GGGTAGTGG GCAGGGAACC 960  
 AGTGTATCC AAGGAGCAGC CTGCGTTCCA GTATAGCAGC CACGTCTCGC TGCAGGCTTC 1020  
 30 CAGTGGGCAC ATGTGGGGCA CGTCCGCTT TGAAAGACCT GATGGCTCCC ACTTTGATGT 1080  
 TCGGATTCTT CCTTCTCCC TGGAAAGCAA TAAAGATGAG AAGACACCAC CCTCAGGCCT 1140  
 TCACTGGTAG GCCAGCTGAG GCCCAAGTG CCCAGGCTTG GTCACCGGGA AGAACAAC TC 1200  
 35 TCATCCACA ATTGCTGCAG AACTCTTCTC TCCCATCAT GGGCCACAGT GGTCTCTTA 1260  
 ATTTGATTGT GCGGTTCTTT TTGTGGGGAG GGTGGTATA ACTTTCTTC AGAAGACCCA 1320  
 40 TGTGGGACAC CTCGAAGGCT GGCCTCCTCA TAAGCCCTGC CTACACCATG TTCCAGTAA 1380  
 CCTCTCCACC AAGGAACTGT GTTCAGCTGC CACAGGCTG GAGGAGTTTC CTGGCCTGTC 1440  
 ACGTGAGGTT TGATCAGTAA ACCAGTGCAS GYTTGCCAA AAAAAAAAAA AAAAAAAAAA 1500  
 45 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAATCGA 1538

50

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AGACCCCTGTC TCAAATAATA ATAATAATRA TAATCTTATT TTGGAGAATA AAGAGACCTS 60  
 TGGATTTGAG GTGCCATTG GGTAGAAAGA AAAGACGTTT ACACCGAGAA ATAGTCTGTG 120  
 5 TTGCCCTGAA GGAGCAGAGG GATGCATCGC TGGAGGTGAC CTACAGTTGA AGAAGACTCA 180  
 TTATGACAGA CCTGTGCTT CTTCCTTGTG GAAAGTGTTT CCTCTGCTGC TACTGCTCAT 240  
 GAGACTCTTC CCCCTCCCTG TCCCAGGGAA CCRAAGGGCT TTNCTACCAC ACCCTTTCTT 300  
 10 NGCCCCCCCC CTCCCATGTC TGCTGTGCCT TTGTACTCAG CAATTCTTNG TTTGCTCCCA 360  
 TTATCTTCCA GCCGGATACA GAGTGAATAG TTAACACAC TTAGGTCAAA TAGGATCTAA 420  
 15 ATTTTGTGTC CTGCTCCNGT GTAAAGAGGC CAGTGTGTTGT GTGTTGCAAG CAGCCTTGGA 480  
 ATAGTAACTC TTCTCATTG TTTGGGATCT GGCCAMCAAG TTCCAGAATG ATACACGGAT 540  
 CAGTGCAGAA GTTCATCAGG CTCTCGGACC TTAGGGCTGT TGGAGAAGGC TTCAGCAGCA 600  
 20 GAACTGATGG TKAWKG/TCG TGTCTCCAT COTCAACTTT CTTTGCTTCG ATCATAACCA 660  
 AGAATACATT TGAAGAGGCA AAAAATGAAC ACTGTTGTTT ATTGCAGCCG TGTTTTGTGA 720  
 25 CACAGATGCA CAGTCTGCTG TGAAGACCTT CTCTCAAGTG GSATYTGGGA GTCCATGCCA 780  
 GATCATGGTG CTTTCATGAGA GACTGACAGC TATCAGGGGT TGTGGCACTT ACTGAGGACT 840  
 CTCCTCCCCC AGTGTGTGCT GATGACACAT ACACACCTGA CAATAGCTTG AGTCTTCTCT 900  
 30 GTTCTTTTTA CTCTGTAGCC AACATACACA TGATTTAAAA CCTTTTCTAA ATATCTATCA 960  
 TGGTTCATCC TTGTCCAAAT GCAGAGTCAG AGCTATTTGT ACTTCATTAT TATTTCCAAG 1020  
 35 GCGAATAGTT GGCTTTCTTT TTGCAAAAAT AATTAAAGTT TTTGTATGTT GCAAAAAAAA 1080  
 AAAAAAAA CTACGTAG 1098

40

(2) INFORMATION FOR SEQ ID NO: 195:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1001 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GAATTCGGCA CGAGATAGCT TGCATCTCAT CCCAGTAAAA CCACTTATTT ATAACATATC 60  
 AACGTATTGA CAAGGTTGAA GAGCAAGATT GTTCTGAGGT GAGATGCCAA TTTCAAAGGG 120  
 55 GTGAGCACTA ATTGTTCCAG TGATTGTTTA TTTATTGGCT AGGACATAAT TACTCTCTTT 180  
 GAGGTTACAC ATCTGCTCC AGGTTCTGT GTGCTTGTGC CCTTGGGATC AGGCCAGGOC 240  
 60 AGACTGTGAT CACTGAGATT CAAACTCCCA GARTATTCAG CAAGAGCTTT CTAGAGACCA 300

AGGCCAGGCC TGATCCCTGA GGGATGCATG AGAAGGCTTG GAATCTCATT CTGCTATGGT 360  
GGCTCTCTCT TGATCTTCTT GGAGTAGCAA AAACAGCAAT GTGGGCCCCA TGGTGTGGCC 420  
5 TAAATGATCA CAAAGGTRAA TGAGTAAAGG GCTCAGCAGA TGAGTAAGGA GCCTTGTCTT 480  
GAGAAATTAG CACTGGGCTC TGCATTGAGA AACATGTGAT AAGCATTGCC CATTGCACAT 540  
10 TGCCTTTTATT GTGTAAGGAC ATGAAATTC AGTTTTGCAT AGCTAGTGAT GAATACCTGA 600  
AGGGAATTGC AGACATATTT TATTTTATTT TTAATTGACA GATGGAATTG TATATATTTA 660  
15 TCATGTACAT AATCATGCTT TAAATATGT ACATTATGGA ATGGCTAAAT CAACTAACC 720  
TAGGCATTAT CTCATATAAT TGTCAATTTT GTGGCGAGAA GACTAAAAAT CTACCCCTTC 780  
AGCATTTTTA AAGAATACAA TGTGTTTAT TAACAACAGT CACCATTGGG TACACTAGAT 840  
20 CTCTTGAACT TCTTCCTCTT ATCTAAGTGA GATCTTGTA CTTTGATAA CAGCTCCCAA 900  
GCCCTTCCCC AACCCTGCT CCACCCGTGG TAACCACCAT TCTATTCTCA ACTTCCTGGT 960  
AATCACCATT CTAGACACAG GGAAGACTCT CTACCCCTCTG A 1001  
25

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

ATAAACTGAA ATAGGTCATG CAAATATAAA ATATTATTTT TAAATTATTT GTCATAAGAA 60  
40 ACGATGGTGG CCATATTTTG CTTTAATAAT GGAAAAAATG TGGTTAGCAT TCTKTGGAAG 120  
GTGGTCATCA GATAGTAGAC ATTTTCTAGG ATTTATTTCT ACCTGCATAT GTGGAAATGT 180  
45 GTACTACTTT AGATTTATWT AATGGCAGCT AACTCAGAGG CATCAAAATG TGCTAATGGT 240  
GTAATATGGC CTTTGTCTTG CTGTCTGTT TTGTARGCCT TCAATCAAGC ARGGGCAGGG 300  
CCGTACAGTG AACTTGTCTT TTGSCAGAGG CCAGCGTCTG CCCCTGACCC CGTCTCCACT 360  
50 CTCTGTGTCC TGGAGGAGGA GCCCCTTGAT GCTACCCCTG ATTCACCTTC TGGTGCCTT 420  
GTACTGAACT GGGAAGAGCC GTGCAATAAC GGATCTGAAA TCCTTGCTTA CACCATTGAT 480  
55 CTAGGAGACA CTAGCATTAC CGTGGGCAAC ACCACCATGC ATGTTATGAA AGATCTCCTT 540  
CCAGAAACCA CCTACCGGTG ACTGCAAGGG AGTAGAAATC TGCATCAGCA CATCAGCACT 600  
TGGGATCTA AGTAAACCTC TCGGGGAAAA TGACCAAGTG GATGTCATCT CCCAGCTGTT 660  
60

	TCTAAGAGCC CAGATGTCCA GAGTACTGTC TCACTTTGAT CCTCAGTTC ABAAGACTTG	720
	TGAAAAAGCC AACTGGTTC AGGCACTCAC TGGACGTTT TGTGTGCACT TTAACATGCA	730
5	CGCTCTCTAC CCCAGAGTGG ACTCAPATCC TCACTTCACT CTCTGAACAT TGGAGTCAGA	840
	AATTATRAAA GGGCTTTGGC AATATGTTAG CCGAAGATT TGGCTTTTC GAAATTTCT	900
10	GCCGACNTTA ACAGTGGCTT AATGATGCT AAACTTTTA AGATTTCTAA AAGTTGGCA	960
	TTGGAGATAC GTTGACTTTT ATTAACMAC CTATGTTCT TTAATGATT CTAAAAAT	1020
	ATCTGGAGCT CAGGGGTTCA ACTGAGGGA CACATTTGA GRATCTTCT TTAATAATTA	1080
15	AATGCCAGGT AACCCGTTGA AATTATCAA AACTTTTTC AGGTACAGA AAGTCTCTA	1140
	GAGGATAGTT CTGTTATGGA GAAGATGAA TGGTTTATA GTGTAGGAC CATGGAAGG	1200
20	TGAGCTTAGA TTTGGATAGT AAAACCTCAA GACCTTACTT AAAAGTATT CTAGCATGC	1260
	AGCATAAATA ATTTAATCA GTGTTAATAT GGCAGGCTA GTATATTGAG CTAAATGCA	1320
	AAAGAACTC ACATGGGAG AATGCCACT TTCTTTATA AGATAGCTT GAATATCCA	1380
25	TTTTAGACAG ATGGAAATG AATAGCTTTA GAAAGGCA AATGTTGATC TTGGGAAA	1440
	AAA	1443

30

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

	GAAAAAAAAA AGTATGACCC AGTAGCTAGG CACCTGTGGC CCGGCCAAT TCAACATAA	60
35	AATTAAGTGT CACAGTATCA TCTTAGAAGT GAAGAAAGCC CTTTATCTT GAACTGCCCC	120
45	TCTACCACCA CCTACTGACA AAGAACATGG TGTATTTGG CATGGGAGAA ATTTCAGTT	180
	TGCTATGGCT TGTATGTGTC CCTCAAAAT CAGTGTTCG CAATGTGCA GATCAAGAG	240
50	GTGGGGTCTT TAAGAGATCA CTAGGCCATG AGGATTTCT TTAGGACTGG GATTAAGCCC	300
	CATAATAAAA GAGGTTTCAG GGAGCATCTT GCTAGCTTGC CTCTGTATG TGAAACACA	360
55	GCAAGAAAGC CCTAGTCAAC AAGTGGCAGC TCTTCACTT TAGACTTTC ATCTCCAGA	420
	ACTGTGAGAA ATACATTTCT GTTCCTTCA AATATCCAG CTCCTGTAT TCTTTATAG	480
	CAGCACAAA TGAAGATACC ATACCTGAC ACCTGACAT TCTTCACAG GAACTAAATG	540
60	CAGTGCTTTA TTCTGGTCTC ACTATGTGT GTTAAATAG GAATGAAA AATTTGGATC	600

450

AGGGCATAGG ATGAACACAGT TACTGCTAGA COTCTCAGAA TGCCACTAAT GGAACAGAT 660  
 GTATTTTCAT CATYNTCTGT CTCTTCGGAA GGTACACCA TGTATATAA GGAATTAAT 720  
 5 AGATGTCTAA AAACACCTTA AGTATTTGTC TGGAACTGT GTCGATGTC GAAAGAAC 780  
 CAAATTCMA AATTAATTCA AAGGGCTAA AGCACTAAT AATCGAAT CATTAATTT 840  
 10 TAATGCTACT ACCACTCTCA AATTTAAAT GTGATCTTA GTTCCTGTC GTGCTATGG 900  
 ATTTATGCT AAAACCTGGT AAACACTTTA ATGCTTTCA ATTCATTA GCTGCTCTT 960  
 GTCCAGAATT ACTCGCAGAC TAATAGTCAC CTGACTTTC CCGCTGATC GGAATTTGT 1020  
 15 GTCTAATCT GTTACAAAT AAGTAACTGC CAACTAATC TTCTAAAAA GGAAGCTCA 1080  
 TCTGCTCACT CTTTGCTCA ACAATGTAA AGTCCCATT GTCTGCTAA TAAACGAGC 1140  
 20 TTCCACTGT GTATACAATA CATCCATGAT CTGTATGAG CATCATTTG TATTGCTCA 1200  
 CTTTATACAC CACCCCCCAT GCCACATCAA ATTAATTAAT CCGATTAAT GGAATGCTA 1250  
 AAAAAAAAAA AAAAAAATC GA 1282  
 25

## (2) INFORMATION FOR SEQ ID NO: 198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

ATTTCCGAAC GAGGACTGAA GTGGGACCG CGCCAGGTA GAGACAGAA GGGGATCTA 60  
 40 TGTGTAACCT AAAGAATGTT TCTGTTTGT TATTATGCT GTGTGTTGG TTTTATGTT 120  
 TGCTTAAGAG AATCAAAAAC TGAATAAAT GAGAATACAG GAAATGGCTC TGTATTATT 130  
 45 TTTGCTGTG TTACAGCTT GTTAATGCTC TACTGTCTT GTTCAAGAG AATTTGTTG 240  
 ACTGCCAGC TCGTTTGTG TCGTAGGCC TAGGCCAGC CCAGCTTATA AATATGCTT 300  
 GTTAGATGT TTGATTTGT TCTGTTTGT ATTGTTATCT TAAGGTGTA TACTCTGAC 360  
 50 ATGCCAGACA TCAATTAAG CTCAAATTAA GCTCTGCTT AATGTTTAA ACCTTAAT 420  
 TATATTCTAA TTGATCCAG CCACTGATGC ATGTACTTTA GCTACTTTC CTAATAAGC 480  
 55 ATATTAAAT TCCACATCAG GCCATCAGAT CTTGAGAAC AACGTTATC TGAATTCGG 540  
 TGTCTACTAA TGTTCACCT GATGCAGCC TTGATTAAT TTGTACAAA ATATAAGTG 600  
 ATCATTATGT AGTTTCTGGA TTAATAAAT TTGTCTGTA AGTTGTTTG CAAATGCT 660  
 60



451

GTGGAATTAA TGGGACAGTG TGCCCTTTGT GTTAGATGTT AGAGCAAAAG AAAGCCCTTA 720  
 TAGTGTAGT ATTGGAGCAC TTGAAGATA GATATTTTCA GAAAGATGT AGGATTTAAA 780  
 5 AGTTAAATTT TAAATTTTAG AAAAGATAT GATGGCAATT GGAATAGTC ACAATGAACT 840  
 TCTTCATCCA GTAGGTGTTT AACAGTGTTA TTTTGCCACT GGTAAATGTTT AAATGTGAG 900  
 10 TGATTTACAA TAAATGATTA TGAATTCAAA AAAAAAAAAA AAAAAACTCG A 951

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TTATTATAAT AATGATGATG ATTCCAAGGA AAAAACCTAC AGCGAATGTT CCAATTTCTAC 60  
 25 CCGGCACCCA GACACTCTCC CTAACACTGA TAACCTGAGC CCCCAGCACT GGACCGAAGA 120  
 ATGCTGGCGT CTCGGTGTGT ACTGGTTCAG GGTTCGGCC CCAGCCTTGT CAGGACCCCC 180  
 30 TGGTGTCCAG AGCCCCCACC CCTCCGCCAA CAAGCAGCTG ATGCCCCAGT GATCTCTAT 240  
 ACATTTTTC A C C T C G G C C A A T A T G T C C A G A A A A C T G C T T A C T C T T T T C T T G C C T G G 300  
 AGCCTTCATT GTTCACCTT ACCTTGCAT ATAGGAATTA ATGCTACAAA ATAAAAAGTAA 360  
 35 AGCTTACCTG AAAAGTCAT AGTTTGGGGC AATGATATCT ACATCTCCCA CTGTGGGAAA 420  
 ACCAGCAAAG CATCAAACT CTCAATCTC CTGTTACCRA ATGCAGATCT GAATTATAAG 480  
 40 ATGTTTATGT TTGACCATG TTTCAACAAT GGGATTTTGT TACGAATTAT CCCTTTAACT 540  
 GAAACCTCA GTTTTACTGT TTACATTATT AGGAAAACAG GGATATCTTT TGAATCTAAA 600  
 AATTTGATGT ACAGCATGTG ATTTTGAAG TTTACATGTA AAGTCACAGT ATAGGTGAAA 660  
 45 TAACGTTTGT CATATTTTGA GAGTATCTT GCAGCCATGT TTTTACGTGA GTGTTTACT 720  
 CAAAGTACAT GGTAGACAGT CTTTCACAAT AAAAGGAAAA GGATTTTTTT TCTCCAAAT 780  
 50 GTACATTTAT CAACCTAATG ATTGATTTTT TAAAAAGAG ATTTGCCCCC AGTCTGGTTT 840  
 ATGAAAGTTC ATTGCCCTAA ACTGTGCTGA TTGTTTTTAA TCAAGTTATA AATTTCCAAC 900  
 55 CTAGATCATG TATCTACCA CTCTCTGCA TTTTCCAAA GGCATTGAGC TTAATATTA 960  
 GTCTTGCTTA GAGTAGGTTA TCCACTTACA TGCTGGGCTA AAGCCATGCC TTTGAAACTC 1020  
 CTGTTTTAAA ACATGATATG ATTTTGTGG GCAGTTTCAG AAAAGAAAAC AAACAAACAA 1080  
 60 AAATCGACCC TTAAATATT ACTTGCAACT CAACAGATCT CCTGCCCTA CTGCTTTTC 1140

5 CAGGAAC TTT ACTTCAGGGC TGTCCAGATT GCAGTGTGTC CCCGTGTATG TGGATCTAGT 1200  
TCACAGAGTC TTTGGAAGCC AGCAGTCGTG CCCTCCGTAT ACTGTCCACT CATT TTTATGT 1260  
AGATTTGGTA TCCTCAGCAG CCAGTGTTAA CACCACTGTC ACGTAGTTAN CAGATTGCATC 1320  
TTTATGTAT TTAAAGTAAT CCATACTATG ATTTGGTTTT TCCCTGCACC ATTAATTCTG 1380  
10 GCATCAGATC AGTTTTTGTG TTGTGAAGTT CTACTGTGGT TTGACCCAAG ACCACAACCA 1440  
TGAGACCCTG AAGTAAAGAT AAGGTACACA TACATTATTT GAGTAACTGT TTCCTTGGGG 1500  
GCCAATCTGT GTATGCTTTT AGAAGTTTAC AGAATGCTTT TATTTTGTG TATAACAAAC 1560  
15 AGTCTGTCTAT TTATTCTGT TGATAAACCA TTTGGACAGA GTGAGGACGT TTGCCCTGTT 1620  
ATCTCCTAGT GCTAACATA CACTCCAGTC ATGAGCGGGG CTTTACAAAT AAAGCACTTT 1680  
20 TGATGACTCA MAAAAAAAAA AAAAAAAAAMC YCGGGGGGGG GCGGTAACC CATTNNCCC 1740

25 (2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

35 GCTTATAGAA GGGAGAGGAG CGAACATGGC AGCGCGTTGG CCGTTTTGGT GTGTCTCTGT 60  
GACCATGGTG GTGGCGCTGC TCATCGTTTG CGACGTTCCC TCAGCCTCTG CCCAAAGAAA 120  
GAAGGAGATG GTGTTATCTG AAAAGGTTAG TCAGCTGATG GAATGGACTA ACAAAGACC 180  
40 TGTAATAAGA ATGAATGGAG ACAAGTTCCG TCGCCTTGTG AAAGCCCCAC CGAGAAATTA 240  
CTCCGTTATC GTCATGTTCA CTGCTCTCCA ACTGCATAGA CAGTGTGTG TTTGCAAGCA 300  
45 AGCTGATGAA GAATTCAGAG TCCTGGCAAA CTCCTGGCGA TACTCCAGTG CATTCAACCA 360  
CAGGATATTT TTGCCATGG TGGATTTTGA TGAAGGCTCT GATGTATTT AGATGCTAAA 420  
CATGAATTCA GCTCCAACTT TCATCAACTT TCCTGCAAAA GGGAAACCCA AACGGGGTGA 480  
50 TACATATGAG TTACAGGTGC GGGGTTTTTC AGCTGACCAG ATTGCCCGGT GGATCGCCGA 540  
CAGAACTGAT GTCAATATTA GAGTGATTAG ACCCCCAAAT TATGCTGGTC CCCTTATGTT 600  
55 GGGATTGCTT TTGGCTGTTA TTGGTGGACT TGTGTATCTT CGAAGAGTAA TATGGAATTT 660  
CTCTTTAATA AAACTGGATG GGCTTTTGCA GCTTTGTGTT TTGTGCTTGC TATGACATCT 720  
GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA 780  
60

453

CATGTGAATT ATATCCATGG AAGCAGTCAA GCCCAGTTTG TAGCTGPAAC ACACATTGTT 840  
 CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAACC TGCTACCTCT 900  
 5 GACATGGATA TTGGAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTGTATTA 960  
 TTCTTCAGTT GGATGCTCTC TATTTTAGA TCTAAATATC ATGGCTACCC ATACAGCTTT 1020  
 10 CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC 1080  
 GAAATCGTG TGTGTTTGA AAGAAGAATG CAACTTGAT ATTTTGATTT ACCTCTTTT 1140  
 TTCAAGTGAT TTAATAGTT AATCATTTAA CCAAGAAGA TGTGTAGTGC CTTAACAAGC 1200  
 15 AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCCTAACCT TCTCTCCCA 1260  
 GTGAACTTTA TGAACATTT AATTTAGTAC AATTAAGTAT ATTATPAAAA TTGTAAACT 1320  
 20 ACTACTTTGT TTTAGTTAGA ACAAAGCTCA AAACACTTTT AGTTAACTTG GTCATCTGAT 1380  
 TTTATATTGC CTTATCCAAA GATGGGGAAA GTAAGTCTTG ACCAGGTGTT CCCACATATG 1440  
 CCTGTTACAG ATAACTACAT TAGGAATTCA TTCTAGCTT CTTCATCTTT GTGTGGATCT 1500  
 25 GTATACTTTA CGCATCTTTC CTTTIGAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG 1560  
 AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC AGCAAGACAG TTGTTTCTCC 1620  
 TCCTCCTTGC ATATTTCTTA CTGAAATACA GTGCTGTCTA TGATTGTTTT TGTMTTGTG 1680  
 30 TTTTTYAGAG ATCAGGTAC TGGGCTC 1707

35

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

45

CTGTCCCCAG TGTTCACAG TAATGACTTG GCACTCCAGA GAAAGTTTCA TCTGTTGCG 60  
 TGTGGTGGCT CCAAGCCAAG CACCTGGCAT GCAGGTCAGC CTTCCCAGC GGGCGTGGCG 120  
 50 TCGTCTCTT CACAGATGCC ACGTTGCAGC CCCAAGGCCT CACCATTTTG CGTTTTTAG 180  
 AAACCCATTT TCTTGGTCAT TTATAAGCT GCTTTATAGA TATCTTTGAT CCTGGCATGC 240  
 55 CTTGGTTTCC TCTCCCTTCC CTCTTCCAA TCCTGGTTTC CTAACCTCCT CTTGTAGTAA 300  
 TTCTCAACTC AACTCAAAGT CCCAAGAATT TGAATGGTA GGATGCTGTG CGGGGAGCTC 360  
 GAGGCTGAGG CATAATCACT GTTTCGGTTC TGCTCATCAG GGGACAGGCT CCCTTACTCA 420  
 60 TGGCAGCCAT GTTTGATTGT CACAGAGCCC CCCGAATACT CTGTCTATAG TGACACACTG 480

TAGGTGTCAT AAATTTTAAG AAACCTGCTT TTAAGTACTA TTTATAGGTT TTTCTGTTAT 540  
 ACTTGCAACC TAGTTTTTAA ATACATGAGG ATTTTATGAA AGCTTTATAC AGACATTTAT 600  
 5 AGGAAACTCA TTCTTTGATT TTAGGTGCCA TTAAATTGA TAACACTTAC TTTATAAAAA 660  
 GATGCTTTTT GTCTGGATAG AGCCTTATAG TTAAATATAT CTTTATATAT TGCCATTTGA 720  
 10 TCAAATAAAT TTCTTACTTA GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAACTCGA 779

15 (2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1617 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

25 GGCACAGCTT TCTGTCTCTT CCTCGCTCCC TCTCTTCTC TCCTCCCTCT GCCTTCCCAG 60  
 TGCATAAAGT CTCTGTGGCT CCCGGAACCT GTTGCCAATG CCTATTTTTT GCCTTTCCCC 120  
 CGCGTTCTCT AAACCTAATA TTTAAAGGTC TGCGGTGCGA AATGGTTTGA CTAAACGTAG 180  
 30 GATGGGACTT AAGTTGAACG GCAGATATAT TTCACTGATC CTCGGCGTGC AAATAGCGTA 240  
 TCTGGTGCAG GCGGTGAGAG CAGCGGGCAA GTGCGATGCG GTCTTCAAGG GCTTTTCGGA 300  
 35 CTGTTTGCTC AAGCTGGGCG ACACATGGCC AACTACCCGC AGCCTGGGAC GACAAGACGA 360  
 ACATCAAGAC CGTGTGCACA TACTGGGAGG ATTTCCACAG CTGCACGGTC ACAGCCCTTA 420  
 CGGATTGCCA GGAAGGGGCG AAAGATATGT GGGATAAACT GAGAAAAGAA TCCAAAAACC 480  
 40 TCAACATCCA AGGCAGCTTA TTCGAACTCT GCGGCAGCGG CAACGGGGCG GCGGGGTCCC 540  
 TGCTCCCGGC GTTCCCGGTG CTCCTGGTGT CTCTCTCGGC AGCTTTAGCG ACCTGGCTTT 600  
 45 CCTTCTGAGC GTGGGGCCAG CTCCTCCCGC GCGCCACCC AACTCACTC CATGCTCCCG 660  
 GAAATCGAGA GGAAGATCCA TTAGTCTTTT GGGGACGTTG TGATTCTCTG TGATGCTGAA 720  
 AACACTCATA TAGGATTGTG GGAATCCTG ATTCTCTTTT TTATTTCGTT TGATTCTCTG 780  
 50 TGTTTTATTT GCCAAATGTT ACCAATCAGT GAGCAAGCAA GCACAGCCAA AATCGGACCT 840  
 CAGCTTTAGT CCGTCTTCAC ACACAAATAA GAAAACGGCA AACCACCCC ATTTTTTAAT 900  
 55 TTTATTTATTA TTAATTTTTT TTGTTGGCAA AAGAACTCA GGAACGGCCC TGGGCACCTA 960  
 CTATATTAAT CATGCTAGTA ACATGAAAAA TGATGGGCTC CTCCTAATAG GAAGGCGAGG 1020  
 AGAGGAGAAG GCCAGGGGAA TGAATTCAG AGAGATGTCC ACGGACGAAA CATACGGTGA 1080  
 60

455

5 ATAATTCACG CTCACGTGCT TCTTCACAG TATCTTGTTC TGATCATTTT CACTGCACAT 1140  
 TTCTCCTCAA GAAAAGCGAA AGGACAGACT GTTGGCTTTG TGTTCGGAGG ATAGGAGGGA 1200  
 10 GAGAGGGAAG GGGCTGAGGA AATCTCTGGG GTAAGAGTAA AGGCTTCCAG AAGACATGCT 1260  
 GCTATGGTCA CTGAGGGGTT AGCTTTATCT GCTGTGTGTT ATGCATCCGT CCAAGTTCAC 1320  
 TGCCCTTTATT TTCCCTGCTC CCTCTTGTTC TAGCTGTTAC ACACACAGTA ATACCTGAAT 1380  
 ATCCAACGGT ATAGATCACA AGGGGGGGAT GTTAAATGTT AATCTAAAAT ATAGCTAAAA 1440  
 AAAGATTTTG ACATAAAGA GCCTTGATTT TAAAAAATA AGAGAGAGAG ATGTAATTTA 1500  
 15 AAAAGTTTAT TATAAATTAA ATTCACCAAA AAAAGATTTG CTACAAAGTA TAGAGAAGTA 1560  
 TAAAAATAAA GTTATTGTTT GAAAAAATA AAAAAAAAW CTCGACCGCA AGGGAAT 1617

20

(2) INFORMATION FOR SEQ ID NO: 203:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1974 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

GAATTCGGCA CGAGGCTGAG GGAGCTGCAG CCGAGCAGAG TATCTGACGG CGCCAGGTTG 60  
 CGTAGGTGCG GCACGAGGAG TTTTCCCGGC AGCGAGGAGG TCCTGAGCAG CATGGCCCGG 120  
 35 AGGAGCGCCT TCCCTGCGGC CGCGCTCTGG CTCTGGAGCA TCCTCCTGTG CCTGCTGGCA 180  
 CTGCGGGCGG AGGCCGGGCC CGCGCAGGAG GAGAGCCTGT ACCTATGGAT CGATGCTCAC 240  
 40 CAGGCAAGAG TACTCATAGG ATTTGAAGAA GATATCCTGA TTGTTTCAGA GGGGAAAATG 300  
 GCACCTTTTA CACATGATT CAGAAAAGCG CAACAGAGAA TGCCAGCTAT TCCTGTCAAT 360  
 ATCCATTCCA TGAATTTTAC CTGGCAGGCT GCAGGCGAGG CAGAATACTT CTATGAATTC 420  
 45 CTGTCTTTCG GCTCCCTGGA TAAAGGCATC ATGGCAGATC CAACCGTCAA TGTCCCTCTG 480  
 CTGGGAACAG TGCCTCACA GGCATCAGTT GTTCAAGTTG GTTCCCATG TCTTGAAAA 540  
 50 CAGGATGGGG TGGCAGCATT TGAAGTGGAT GTGATTGTTA TGAATTCTGA AGGCAACACC 600  
 ATTCTCCAAA CACCTCAAAA TGCTATCTTC TTTAAACAT GTCAACAAGC TGAGTGCCCA 660  
 GCGGGGTGCC GAAATGGAGG CTTTGTGAAT GAAAGACGCA TCTGGGAGTG TCCTGATGGG 720  
 55 TTCCACGGAC CTCACTGTGA GAAAGCCCTT TGTACCCAC GATGTATGAA TGGTGGACTT 780  
 TGTGTGACTC CTGGTTTCTG CATCTGCCCA CCTGGATTCT ATGGAGTGAA CTGTGACAAA 840  
 60 GCAAACTGCT CAACCACTG CTTTAATGGA GGGACCTGTT TCTACCTGG AAAATGTATT 900

456

TSCCCTCCAG GACTAGAGGG AGAGCAGTGT GAAATCAGCA AATGCCCAACA ACCCTGTGGA 960  
 AATGGAGGTA AATGCATTGG TAAAAGCAAA TGTAAGTKTT CCAAAGGTTA CCAGGGAGAC 1020  
 5 CTCTGTTCAA AGCCTGTCTG CGAGCCTGGC TGTGGTGCAC ATGGAACCTG CCATGAACCC 1080  
 AACAAATGCC AATGTCAAGA AGGTTGGCAT GGAAGACACT GCAATAAAAG GTACGAAGCC 1140  
 10 AGCCTCATAC ATGCCCTGAG GCCAGCAGGC GCCCAGCTCA GGCAGCACAC GCCTTCACCT 1200  
 AAAAAAGGCG AGGAGCGGCG GGATCCACCT GAATCCAATT ACATCTGGTG AACTCCGACA 1260  
 TCTGAAACGT TTTAAGTTAC ACCAAGTTCA TAGCCTTTGT TAACCTTTCA TGTGTTGAAT 1320  
 15 GTTCAAATAA TGTTCAATAC ACTTAAGAAT ACTGGCCTGA ATTTTATTAG CTTCATTATA 1380  
 AATCACTGAG CTGATATTTA CTCTTCCTTT TAAGTTTCTT AAGTACGTCT GTAGCATGAT 1440  
 20 GGTATAGATT TTCTTGTTTC AGTGCTTTGG GACAGATTTT ATATTATGTC AATGATCAG 1500  
 GTTAAATTT TCAGTGTGTA GTTGGCAGAT ATTTTCAAAA TTACAATGCA TTTATGGTGT 1560  
 CTGGGGGCG GGAACATCA GAAAGGTTAA ATTGGGCAAA AATCGTAAG TCACAAGAAT 1620  
 25 TTGGATGGTG CAGTTAATGT TGAAGTTACR GCATTTTACA TTTTATTGTC AGATATTTAG 1680  
 ATGTTTGTTA CATTTTAAA AATTGCTCTT AATTTTAAA CTCTCAATAC AATATATTTT 1740  
 30 GACCTTACCA TTATTCCAGA GATTCAGTAT TAAAAAATA AAAATTACAC TGTGGTAGTG 1800  
 GCATTTAAAC AATATAATAT ATTCTAAACA CAATGAAATA GGAATATAA TGTATGAAT 1860  
 TTTTGCATTG GCTTGAAGCA ATATAATATA TTGTAAACAA AACACAGCTC TTACCTAATA 1920  
 35 AACATTTTAT ACTGTTTGTA TGTATAAAAT AAAGGTGCTG CTTAGTTTT CTGA 1974

40

(2) INFORMATION FOR SEQ ID NO: 204:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

55

60

CGGCCTTCCG GGGCAACCGT TCGTCCCAAC NCGGGAAGG GTCCTGGAGN CGGGAAC TAG 60  
 GAGCCTCGGA AGTCCAAGGG CGGAGCGCCC TTTGCTAATA AGCCAATCAG AACGTGAGAC 120  
 GCTCCGGTGG GNCGGTGCCG TCGACCGCGG GGTGGAGTCT GGGTGACTTG GCTGGCGGGA 180  
 TCAAGTGCAG CTGCTTCAGG CTGAGGTGGC AGATAGTGAG CGCTGGTGGC GGAGTTAAAG 240  
 TYAAAGCAGG AGAGTAATWA TGAATAGCGC AGCGGGATTG TCACACCTAG ACCGTCCGGA 300

457

GCGGGTTCTC AAGTTAGGGG AGAGTTTCGA GAAGCAGCCG CGCTGCCCTT CCACACTGTG 360  
 CGCTATGACT TCAAACCTGC TTCTATTGAC ACTTCTTCTG AAGGATACCT TGAGKTTGGC 420  
 5 GAAGKTGAAC AGKTGACCAT WACTCTGCCM AATATAGAAA GTTGAAGGAA GCAGTAAAAT 480  
 TCAGTATCGT AAAGAACAAC AGCAACAACA ATGTGGAATT CAGCCAGGAC TCCCAATCTT 540  
 GTAAAACATT CTCCATCTGA AGATAAGATG TCCCCAGCAT CTCCAATAGA TGATATCGAA 600  
 10 ACAGAACTGA AGGCAGAAGC TAGTCTAATG GACCAGATGA GTAGTTGTGA TAGTTCATCA 660  
 GATTCCAAAA GTTCATCATC TTCAAGTAGT GAGGATAGTT CTAGTGAATC AGAAGATGAA 720  
 15 GATTGCAAAT CCTCTACTTC TGATAAGGGG NAATTGTGTC TCAGGACATC CTACCATGAC 780  
 ACAGTACAGG ATTCTTGATA TAGATGCCAG TCATAATAGA TTTCCAGACA ACAGTGGCCT 840  
 TCTGATGAAT ACTTTAAGAA ATGATTTGCA GCTGAGTGAA TCAGGAAGTG ACAGTGATGA 900  
 20 CTGAAGAAAT ATTTAGCTAT AAATAAAAAT TTATACAGCA TGTATAATTT ATTTTGTATT 960  
 AACAATAAAA ATTCCTAACA CTGAGGGAAA TATGTCTTAA CTTTGTATGA TAAAAGAAAT 1020  
 25 TAAATTTGAT TCAGAAAAAA AAAAAAAAAA AACTCGA 1057

30 (2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

40 GAATTCGGCA CGAGTCATCC CTCTCCCTCT TTCACTCCCT TACTCTTACT CTGTTTTTTG 60  
 TGCTCCAGAC AGACAGACCC TACCTCTTTT GCTTCTTTTT TGTGTTGTTG TTTTGAGATG 120  
 GAGTGTGGCT CTTGTTGCCC AGGCTGGAGT GCAGTGGCCG AATCTCGGCT CACCACAACC 180  
 45 TCTGCCCTCC GGGTTCAAGC AATTCTCCTG CCTCAGCCTC CCGAGAAGCT GGGGATTACA 240  
 GGCATGCGCC ACCACACCCA GCTNAATTTT ATATTTTTAG TAGAGATGGT GTTCTCCAT 300  
 50 GTTGGTCAGG CTGGCTCAA ACTCCCAACC TCAGGTGATN CCGCCTGCTT TGGCCTCCCC 360  
 AAAGTGCTGG GATTACAGGC GTGAGCCACT GCGCCAGCC TCTTTTGCTC CTTTATACTC 420  
 ATTAACACAC GCGTGAATC CCGTTTGTG GAGGCCAAAG TGAGAAGGTT GCTTGAGGCC 480  
 55 AAGAGTTTGA GACTAGCCTG GGCAACACAG CAGATGCCA TCTTTATAAT AAAAATAAAA 540  
 ATAAAAATCA ATTAGCTGGG CATGGTGCAA CGCACCTGTA GTCCCAGCCA ATGAGAGGCC 600  
 60 TGAAGTGGGA GGATCATGA GCCCAGGAGT TGAGGTTGCA GTGAGCCATG ATCATGTGAC 660

TACACTCAGC CTGGGCAATA GAGGGACATG TTGTCTCTAA AAAAAAAAAA AAAAAACTCG 720

A 721

5

(2) INFORMATION FOR SEQ ID NO: 206:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

20

CCACGATTTA TCCAAGTGA GAGGAGTTAC AGGCAGTTCA GAAAATTGTT TCTATTACTG 60

AACGTGCTTT AAAACTCGTT TCAGACAGTT TGTCTGAACA TGAGAAGAAC AAGAACAAAG 120

ACGGAGATGA TAAGAAAGAG GGAGGTAAAG ACAGAGCTTT GAAACGAGTT TTGCGAGTGG 180

25

GAGTATTGGC AAAAGGATTA CTTCTCCGAG GAGATAGAAA TGTCAACCTT GTTTTGCTGT 240

GCTCAGAGAA ACCTTCAAAG ACATTATTAA GCCGTATTGC AGAAAACCTA CCCAAACAGC 300

30

TTGCTGTTAT AAGCCCTGAG AAGTATGACA TAAATGTGC TGTATCTGAA GCGGCAATAA 360

TTTTGAATTC ATGTGTGGA CCCAAATGC AAGTCACTAT CACACTGACA TCTCCAATTA 420

TTCCGAGAACA GAACATGAGG GAAGGAGATG TAACCTCGGG TATGGTGAAA GACCCACCGG 480

35

ACGTCTTGA CAGGCAAAAA TCCCTTGACG CTCTGGCTGC TCTACGCCAC GCTAAGTGGT 540

TCCAGGCTAG AGCTAATGGT CTGCAGTCCT GTGTGATTAT CATACGCATT CTTCCGAGCC 600

40

TCTGTGAGCG AGTTCCAAC TGGTCTGATT TTCCAAGCTG GGCTATGGAG TTAGTAGTAG 660

AGAAAGCAAT CAGCAGTGCT TGTAGCCCTC AGAGCCCTGG GGATGCACTG AGAAGAGTTT 720

TTGAATGCAT TTCTTCAGGG ATTATTCTTA AAGGTAGTCC TGGACTTCTG GATCCTTGTG 780

45

AAAAGGATCC CTTTGATACC TTGGCAACAA TGACTGACCA GCAGCGTGAA GACATCACAT 840

CCAGTGCACA GTTTGCATTG AGACTCCTTG CATTCGCGCA GATACAGAA GTTCTAGGCA 900

50

TGGATCCATT ACCGCAAAATG AGCCAACGTT TTAACATCCA CAACAACAGG AAACGAAGAA 960

GAGATAGTGA TGGAGTTGAT GGATTTGAAG CTGAGGGGAA AAAAGACAAA AAAGATTATG 1020

ATAACTTTTA AAAAGTGTCT GTAAATCTTC AGTGTTAAAA AAACAGATGC CCATTTGTTG 1080

55

GCTGTTTTTC ATTCAATAA ATGTCTACAT TGAAAAATTT ATCAAGAATT TAAAGGATTT 1140

CATGGAAGAA CCAAGTTTTT CTATGATATT AAAAAATGTA CAGTGTTAGG TATTATTTGA 1200

60

ATGSAAGAC ACCCAAAAAA AAAAATGTGC TCCGACTAGG GGGAAAACAG TAGTTCCGAT 1260



459

	TTTTTCCCAT TATTTTATT TTATTTCTG GTTGCCCTAG CTTCCCCCCT TATTTTGTG	1320
	TCTTTTATTA ACTAGTGCAT TGTCTTATTA AATCTTCACT GTATTTAATG CAGGATGTGT	1380
5	GCTTCAGTTG CTCTGTGTAT TTGATATTT TAATTTAGAG GTTTTGTGTG CTTTTTGACA	1440
	CTAGTTGTAA GTTACTTTGT TATAGATGGT ATCCTTTACC CCTTCTTAAT ATTTTACAGC	1500
10	AGTACGTTTT TTGTAAAGT GAGACTGCAG AGTTTGTTTT TCTATATGTG AAGGATTACA	1560
	ACACAAAAAG TTATCCTGCC ATTCGAGTGC TCAGAACTGA ATGTTTCTGC AGATCTTGTG	1620
	GCATTTGTCT CTAGTGTGAT ATATAAGGT GTAATTAAGA CAGAGTTCTG TTAATCTAAT	1680
15	CAAGTTTGCT GTTAGTTGTG CATTAGCAGT ATAAAAGCTA ATATATACTA TATGCTCTTG	1740
	CAACAGTTTT AAAGCCTCTG CATAATTGAT AATAAAAATG CATGACATTC TTGTTTTTAA	1800
	TAGACTTTTA AAATCATAAT TTAGGTTTA ACACGTAGAT CTTGTACAG TTGACTTTTT	1860
20	GACATAGCAA GGGCAAAAAT AACTTTCTGA ATATTTTTTT CTTGTGTATA AGTGGAAAGG	1920
	GCATTTTCA CATATAAGTG GGCTAACCAA TATTTTCAA AGAACTTCAT CRTGTACAA	1980
25	CTAACACAG TAACTAGCCC TTAATTATGG TCACAGTTCC TTATGCTGT GTGTGAGATT	2040
	ACTCTAGCAA CTATTACAGT ATAACACAGA TGATCTTCTC CACACACCCC ATCACCACAG	2100
	TAATTTACAG TTCTGTTAAC AGTGAGGTTG ATAAAGTATT ACTGATAAAA AATTATCTAA	2160
30	GGAAAAAAC AGAAAATTAT TTGGTGTGGC CATCTTACCT GCTTATGTCT CCTACACAAA	2220
	GCTAAATATT CTAGCAGTGA TGTAAAGAAA AATTACATCT TACTGTTGAT ATATGTATGC	2280
35	TCTGGTACAC AGATGTCATT TTGTTGTCAC AGCACTACAG TGAATACAC AAAAAATGAA	2340
	ATTATATAAA TGACTTAAAT GTATTATATG TTAGAATTGA CAACATAAAC TACTTTTGCT	2400
40	TTGAAATGAT GTATGCTTCA GTAAAATCAT ATTCAAATTT AAAAAAAAAA AAAAAAAAAA	2460
	CTCGA	2465

45

(2) INFORMATION FOR SEQ ID NO: 207:

	(i) SEQUENCE CHARACTERISTICS:
50	(A) LENGTH: 1480 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:
----	--

	GAATTCGGCA CGAGCTCAAG CTGGCAGGTG GTGGGGGGAG CGGGCGGAGA GGAGCTGCCG	60
	GGAGTTCGTG CCTGCGAGGA CATGACACCA GTGGCATATC ACGGCCATGG GGTCTCAGCA	120
60	TTCCGCTGCT GCTCGCCCTT CTTCTGCGAG GCGAAGCAA GAAGATGACA GGGACGGTTT	180

	GCTGGCTGAA CGAGAGCAGG AAGAAGCCAT TGCTCAGTTC CCATATGTGG AATTCACCGG	240
5	GAGAGATAGC ATCACCCTGTC TCACGTGCCA GGGGACAGGC TACATTCCAA CAGAGCAAGT	300
	AAATGAGTTG GTGGCTTTGA TCCCACACAG TGATCAGAGA TTGCGCCCTC AGCGAACTAA	360
	GCAATATGTC CTCCTGTCCA TCCTGCTTTG TCTCCTGGCA TCTGGTTTGG TGGTTTTCTT	420
10	CCTGTTTCCG CATTCACTCC TTGTGGATGA TGACGGCATC AAAGTGGTGA AAGTCACATT	480
	TAATAAGCAA GACTCCCTTG TAATTCTCAC CATCATGGCC ACCCTGAAAA TCAGGAACTC	540
15	CAACTTCTAC ACGGTGGCAG TGACCGCCT GTCCAGCCAG ATTCAGTACA TGAACACAGT	600
	GGTGAATTTT ACCGGGAAGG CCGAGATGGG AGGACCGTTT TCCTATGTGT ACTTCTTCTG	660
	CACGGTACCT GAGATCCTGG TCCACAACAT AGTGATCTTC ATGCGAACTT CAGTGAAGAT	720
20	TTCATACATT GGCCTCATGA CCCAGAGCTC CTTGGAGACA CATCACTATG TGGATTGTGG	780
	AGGAAATTC ACAGCTATTT AACAACTGCT ATTGGTTCTT CCACACAGCG CCTGTAGAAG	840
25	AGAGCACAGC ATATGTTCCC AAGGCCTGAG TTCTGGACCT ACCCCACCT GGTGTAAGCA	900
	GAGGAGGAAT TGGTTCATT AACTCCCAGC AACATCCTC CTGCCACTTA GGAGGAAACA	960
	CCTCCCTATG GTACCATTTA TGTTCCTCAG AACCAGCAGA ATCAGTGCCT AGCCTGTGCC	1020
30	CAGCAAATAG TTGGCACTCA ATAAAGATTT GCAGAATTTA ATACAGATCT TTTCAGCTGT	1080
	TCTTAGGGCA TTATAAATGG AAATCATAAC GTGGTTCTAG GTTATCAAAC CATGGAGTGA	1140
35	TGTGGAGCTA GGATTGTGAG TGACCTGCAG GCCATTATCA GTGCCTCATC TGTGCAGAAG	1200
	TGCAGCAGA GAGGGACCAT CCAATACCT AAGAGAAAAC AGACCTAGTC AGGATATGAA	1260
	TTTGTTCAG CTGTTCCCAA AGGCCTGGGA GCTTTTGA AAGAAAGAAA AAAGTGTGTT	1320
40	GGCTTTTTTT TTTTITAGAA AGTTAGAATT GTTTTACCA AGAGTCTATG TGGGGCTTGA	1380
	TTCAACCCTC ATCCATGGC TGAACATGG ATTGGGATT TGATAGAAA ATAAACCCTG	1440
45	CTTTTGATT AAAAAAAAAA AAAAAWAAA AAAAATCGA	1480

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CAGTATTTCC CTCAGTACTG TAAGCAAAG TGSTATGTTT TTCTTCTTT ATGTCTACTC

60

5  
 10  
 15  
 20  
 25  
 30

TGTCTCTGT GGCCTTCTGG TGTACCCCTC TCTTCTAGC CATTTCAGTCT CTCTAGTCAC 120  
 CTCCTTAGTA GCTAGTGCTC TCTAAGTTT TATTTAATTA GAACAACTCC ATTTCCATTT 180  
 CAAGGTAGGT CAATGGGGGG AAAAGCCTCA TGATTTAAAC TGAAGTTAAC AACACAGCTT 240  
 TTAATAATGAA AACTCATACT CCAACTTCTA AAGTATATTT GAGCTGATTT GTTTCCAAAA 300  
 CAAAGATATG CTGTACCTAA AACTGCTAAA ACAAAAATAT AAAGACAAGG ACTAGGTGAT 360  
 TAAGGGGACA GAAAAATCAT VTCTTTTCCA GGAAACCTTT GCTAAAATAA GCAAAACTTG 420  
 ANTCTATGCT TCATGGAAAC TGACACAAAG AAAAGAACT GATGGATTGC ACAGGCCTTG 480  
 TTATAGAAAT AGATCTATAA AAAGATCTGT CCACAGGAAA TATACACCTT CTCCTGGTTC 540  
 TGAACCTCAA TGGGGATTG TCACCTAGGT CTCCATCTAT AGGAATACCT TCACATACCT 600  
 ATCTATTCAT GCACATATTC TGAAAACAGG TACATACAAA ATTACAACAA AGGAAAAAAA 660  
 TTCTATTGAA CACTTAAAAA TAGAAACAGG CCAGGCACGG TGGCTCATGC TGTAATCCCA 720  
 ACAATTTGGG AGGCTGAGGC TGGTGGATCA CCTGAGGTCA GGAGTGTGAG ACCAGCTTGG 780  
 CCAACATGGT GAAACCCCGT CACTACTTAA AATACAAAAA AAATTAGCCT GTGTGGTGGC 840  
 ACACTCNTAC AATCCNGGCT GACTCGGGAA AN 872

## (2) INFORMATION FOR SEQ ID NO: 209:

35  
 40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1779 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

45  
 50  
 55  
 60

AATTGCCAAG ACTGCACAAA ATTACAGTGC TAATGTATAT GGTTGCAGTT CACATAAAGA 60  
 CAAAAGCATC TGTATGAAA TGAGTAGTAA TATTGGGTGG TTGATTGTT CTTAGCAGAC 120  
 TTGGCTTCAT WTGGTCTTG AGATAAAATG GCCAGCATAA ATGCTGTTTA TATTQACGTT 180  
 TTCTAGGTG TGTGTGTGCA GGCCACAGCA GCAAGCCCTT GGTGTAGTCA GTGCCGAAAS 240  
 GGGTCTGTTT CTCTTTGAGC CTGCCTGCAG GGATGGTCTC CTTTTAAAGC AGGTTGTGTG 300  
 CAGCATTCAG TACACTGAAG GTAAGCTAAA CCATCAACAT CTCTGGTGT TTAAGATGTT 360  
 ATTTTATTGG AACAACTGAC AAATGAGGGA TGTTAGCTTT GTGGCAGAAT TCCCTGCATG 420  
 TGTGATAACT GATCTTGT TTATTTTGG CATTGCAACT GTGGCATAGT TACAATTTCT 480  
 GTTTGATCAT CACATTTAAA ATGGRAGAG AACGGGCTTG AAGGATAGAG GGCCTTCAGK 540  
 GTACTGTTTC TTATTAACCT TACTTTTTTT AAATCAACTT GCTATAGACT TTATATACAT 600

5 TTTGTTAAAT ATAGTTCCTA GTGACATAGA AACGATCCGT AGTTTTTCATT TACTAATTAC 660  
 AAATGTTGAG GCCTAATTCT GAAAGTCCTC ATATTTAAAG GCTAGACAAC GTAATGAAT 720  
 TTTTAACTAT TTGTATGTCA TTTTGAAAGT GTACTGCTTT ATGGTAAAAG TGTTTTTCAT 780  
 TTGTTTCATTG TTTTCATTAT TTGTGATCAT GTTGTCTTTC AATACAGGCA TAAACCTTCC 840  
 10 ACTCTTGAAC AAAGCAGCTG CTTTTTAAAA GCGGTAATTG CTTCTTTACC TTTTATTTCT 900  
 TTTGTAAATG AAGCTTTTCT TTAAGAATGT GACTTTAAAG TGTGTCTAT TGCATAAAAC 960  
 AGTTGACACT CACTTATTGT AAAGTGAAGA TTGTTCTACT GCATGTGAAG TGGACCATGC 1020  
 15 AGATTTCTGT ATGTTCTCAG TATGCATCAC TAGATAATAA AGTCTTTTGT GAACAAGGCA 1080  
 TTTGTAGCCA TTTTAAAG TTTTGTCTT CAGTGCTGGT AAGTCAGGTA AACCATAAAT 1140  
 20 AGTTAAAAGC AACCTTTTGT TTTTTTCTG AAAGTTTTTA ATTGAAAGTA TTATTAGTTA 1200  
 AAGATGTAAA CCTAGCCAAA ATTACCAGTT TATTAATAAT TAGGATCCTA ATTATTTCAA 1260  
 AAAATCCTAC AAATATTGTC AGCTTTCAGT GTAGTGAGAT TATTCCTGTA GGTATATGGG 1320  
 25 TATAATTGAG GATTTAACTA ATGTTTCTGC TATTTTCTCA CTTTCTCTT TGATGGTGCG 1380  
 GAAAGAGAAA AAGGAAAACG GGGCACAGGC CATTCGACGC CTTCTCCAAG GGGTCTGATT 1440  
 30 TGCTGAGACA CCAGCTTCAC CTTCTTAACA AGGCACCTAA TTACAACAAG CATGCACATT 1500  
 TTGGTGCAAT CAAGAATGGA AAATCAGAAT AGCAGCATTG ATTCTTCTGG TGCAGCTCAG 1560  
 TCGAAGATGA TGACAACCAG AAGACATGAG CTAAGGGTAA GCGACTGTTT TGAAGAACCT 1620  
 35 TTCCATTTAG TGATCAAGAT ATGGAAGCTG ATTTCTGAAA ATGCTCAGTG TGTACTCTAA 1680  
 TTATTTATGG TACCATTGTA ATTGTAACCT GCATTTIAGC AGTGCAATGT TCTAATTGAC 1740  
 40 TTACTGGGAA ACTGAATAAA ATATGCCTCT TATTATCAA 1779

45 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 2110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

55 GCGGCCCTG CAGCCCGGAG CTGAGCTAGC CGTCCGAGCC GAGCCGTCCG AGCCCGGGAA 60  
 GCCGGCGCGT GCTGCCGCTC GTGGCGGCCA GAGGAGAGGA GAGSCAGCAG CATGGCGAGT 120  
 60 GTCCTGTCCC GACGCCTTGG AAAGCGGTCC CTCCTGGGAG CCGGGGTGTT GGGACCCAGT 180

	GCCTCGGAGG GGCCTCGGCT GCCCCAGCCT CGGAGCCACT GCTAGAAGGG GCCGCTCCCC	240
	AGCCTTTCAC CACCTCTGAT GACACCCCTT GCCAGGAGCA GCCCAAGGAA GTCCTTAAGG	300
5	CTCCCAGCAC CTCGGGCCTT CAGCAGGTGG CCTTTMAGCC TGGGCAGAAG GTTTATGTGT	360
	GGTACGGGGG TCAAGAGTGC ACAGGACTGG TGGWGCAGCA CAGCTGGATG GAGGGTCAGG	420
10	TGACCGTCTG GCTGCTGGAG CAGAAGCTGC AGGTCTGCTG CAGGGTGGAG GAGGTGTGGC	480
	TGGCAGAGCT GCAGGGCCCC TGTCCCCAGG CACCACCCCT GGAGCCCGGA GCCCAGGCCC	540
	TGGCCTACAG GCCCGTCTCC AGGAACATCG ATGTCCCAAA GAGGAAGTCG GACGCATGGA	600
15	AATGGATGAG ATGATGCCGG CCATGGTGCT GACGTCCCTG TCCTGCAGCC CTGTTGTACA	660
	GAGTCTTCCC GGGACCGAGG CCAACTTCTC TGCTTCCCGT GCGGCCTGGG ACCCATGGAA	720
20	GGAGAGTGGT GACATCTCGG ACAGCCGCAN CAGCACTACC AGCGGTCACT GGAGTGGGAG	780
	CAGTGGTGTC TCCACCCCTT CGCCCCCCCA CCCCCAGGCC AGCCCCAAGT ATTTGGGGGA	840
	TGCTTTTGGT TCTCCCAAA CTGATCATGG CTMTGAGACC GATCCTGACC CTTCCTGCT	900
25	GGACGAACCA GCTCCACGAA AAAGAAAGAA CTCTGTGAAG GTGATGTACA AGTGCCCTGTG	960
	GCCAACTGTG GGCAAAGTTC TGCGCTCCAT TGTGGGCATC AAACGACACG TCAAAGCCCT	1020
30	CCATCTGGGG GACACAGTGG ACTCTGATCA GTTCAAGCGG GAGGAGGATT TCTACTACAC	1080
	AGAGGTGCAG CTGAAGGAGG AATCTGCTGC TGCTGCTGCT GCTGCTGCCG CAGACCCCCA	1140
	GTCCCTGGGA CTCCACCTC GCAGCCAGCT CCCACCCCCA GCATGACTGG CCTGCTCTG	1200
35	TCTGCTCTTC CACCACCTCT GCACAAAGCC CAGTCTCCG GCCCAGAACA TCCTGGCCCG	1260
	GAGTCTTCCC TGCCCTCAGG GGCTCTCAGC AAGTCAGCTC CTGGGTCTTT CTGGCACATT	1320
40	CAGGCAGATC ATGCATACCA GGCTCTGCCA TCCTTCCAGA TCCAGTCTC ACCACACATC	1380
	TACACCAGTG TCAGCTGGGC TGCTGCCCCC TCCGCGCCT GCTCTCTMTT TCCGCTCCGG	1440
	AGCCGGTGGC TAAGCTTCAG CGAAGCCCCA GCAGCCAGCA CCTGCGATGA AATCTCATCT	1500
45	GATCTGCACT TCTCCACCCC GGGCCAGAG TGGTGCCAGG AAAGCCCGAG GGGAGCCTAA	1560
	GAAGTGCCGC AAGTGTATGG CATCGAGCAC CGGGACCACT GGTGCACGGC CTGCCGGTGG	1620
50	AAGAAGGCCT GCCAGCGCTT TCTGGACTGA GCTGTGCTGC AGGTCTACT CTGTTCTCTG	1680
	CCCTGCCGGC AGCCACTGAC AAGAGGCCAG TGTGTACCA GCCCTCAGCA GAAACCGAAA	1740
	GAGAAAGAAC GGAACACGG AGTTTGGGCT CTGTTGGCTA AGGTGTAACA CTAAAGCAA	1800
55	TTTTCTCCCA TTGTGCGAAT ATTTTATTTT TTAACAAAAA GAAACAAAAA TATTTTCCC	1860
	CCTAAATAG GAGAGAGCCA AACTGACCA AGGCTATTCA GCAGTGAACC AGTGACCAA	1920
60	GAATTAATTA CCCTCCGTTT CCCACATCCC CACTCTCTAG GGGATTAGCT TGTGCGTGTC	1980

AAAAAGAGGA ACAGCTCGTT CTGCTTCCTG CTGAGTCGGT GAATTCCTTG CTTTCTAAAC 2040  
TCTTCCAGAA AGGACTGTGA GCAAGATGAA TTTACTTTTC TTAACAAAAA AAAAAAATAA 2100  
5 AAAAAGCTGA 2110

10 (2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20 GGCACAGGAA AAAAAAGAAA AAAGAAAAAA GAAAAAGTT TTTGTACCCA CAGATTAGCA 60  
TTTTCTTGAT GTTTGAAAAA AGTTTAAGCT ATGTCTAAT TTAACAAATGA GCACAAACTA 120  
CTTAACAGAT GTCTGTCCC TCTCTCTTA CTTAAATTAT CTTTATTTTC ACCATCACCT 180  
25 CCCAGTGCCG AACACCTGAN CTCTGTGTTT TGTGGTTGGA TCCTGGGTG CCAAGTTCCT 240  
ATTTGGTCAG TCCCTGGCCT GTGGGGCGGT CTCAGGAAGT GGCATGCTCT TCAMGRAGGA 300  
30 TCGTTCATYT CCAGTATAAC CAAATTGTTA ATAATAGTTG ATAATCCCA GCTTTTACCA 360  
GATGATTTTT GACTTATTTT TCCTCCTTTG ACCTGTTCAA AGCTAACATA TCTCGGTCAG 420  
TTGGGAGAGG GTGGGGGATT TGAGAATGTG AGGAGGAGTG GGGTTAGAAT GGGTTTGCCT 480  
35 ATCTGGGCAA GGAAAGAGTT CCTAGTCGAT TGGGCACAAT GACAAATGA TTCCATGGAT 540  
AGAATCGTCC CATGTTGCTG GAACACCTCA CGTGTGTGTA ACGCCTTAAA TTCCTGCCAT 600  
40 CCCTTCTCTG ATTCCCACCC TCCCTGTAGT TTCCACAGGA TTTATCTCTC TGTACCCCCG 660  
TCCTCCAAT CTACTCTGTC AGCCTCTCCT CCATCCCTTA CTTCCCTTCT AAATTCAGG 720  
AGATGACCTC ACTTTGCAAA GCAAAATGGA GCCACCAAT TGTAGCTCTC CTCGGTGGAA 780  
45 ACTGCATCTG TGCTCATCCC TGCACCTTCT TGCAGAAAGC CGCCCCCTCA GGCCAAGATG 840  
AGTGCCTGGC CCCCATGGGA GACTCAGACA CTTTGACCCC TTGTGACTTC AGCATCTCCC 900  
50 TCTTTAAAGA TTCTCTCCCA ACATTCACTC GTGCTCGA 938

55 (2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1551 base pairs  
(B) TYPE: nucleic acid  
60 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

5	AGGCTGGACT AAGCATAGAG AACCAGGAGA GAAAGAAACA TTAAAGAGAC TGGTATATAT	60
	TTTTTGACAG ATCATTTAAG AAACAGAGTA ATTTTTTTTT TCTCCAAAAG GGCATGGGTT	120
10	TTTTTTTGT TTGTTTTTTT CTCTATTTGG CACTTTCTAG GGATTGGTCT ATAAATTTTT	180
	TGAAAGATCA TAGGATAAAT TTCTTTGTAG CAACTTCCTA TTTTAGTCTT TATGTTAGGG	240
	GARCCCCARG TGTCCCTGCT GATACGCCAT TAGGGCCACT TCTCAGCCTC TGGCTACATC	300
15	ATAATGCTTT TTTTCTATC TTGCCAAAGT TTCCMGAAAA TTKAKGTTTT CTATTTTTAA	360
	AAAAATGGT TGTGGAGATG GGATGGGACC TCTTTATAAG CCCTGAAAAT AAGTGTITTN	420
20	TTTTAAGTGC TATCTGCTA TAAACCTGAT TCTCACTTTT TTCTGTAGAC AACGTTTTTT	480
	TATAATATAT CTATTTTGTG TGGACATTAT TTCCTTTTAA CCAATACTGA AATTCCATAG	540
	TGTAWACTTT CTCCACATTT TCTTTGATTA ATACTTCTT AAAATAGACA CTGGGATTGG	600
25	CACCAGCTGT CACCAATAAA GCTGCCCTGA ACATTGTCAA TCAATCCTGT TAACCAATTT	660
	GAGAAATTTT CTGGAATGCT TAGTTAGGGA TGAAATGCT GGGTTATAGG TATGAGTATG	720
30	CTTGATATAC TTTCTCCAG AATGTCTACA CCTGTGTGTA CACCACATCT CCAGAGATAG	780
	GGGAATCTTA TGTCCCTGCT AACTGCTCTC GTTATTTAAT TTTCTGACAT TTGCCGCCCC	840
	CGCCGCCCCC TGCCCCAAC ACACACATGG TATAAAGTGG TAGTTTCTTG TTTTAAATG	900
35	AACTTTTGAA TGATTTGAAT TTGGGCATTT CTMTGTATCC TGAGTTATTT TGCTTTCCCG	960
	TTATGTGAAT ATCCTTTTCC TATGCTTTAA CTACTTTTCT AATTTGTCCC TTTTTTNGGT	1020
40	TATCAAATTC CAGGCCATG TCTATTCCTAT CGTCACTTTT GGGTATGGA AACATCTTTC	1080
	CATTCTGTAG CCTGTCTGTT GAACATAAAT CTGTATTTT ATGTAATCAG ATTTTCTCTC	1140
	TTACGTTAT GTTCTTGGAA TTTTATTTAA GAAATCTTT TCTATCCTGA GACCACAAA	1200
45	ATGTCCCCAC CATTTCTTC TGTTCATAG TTTTGCCTG TATGTTAAT CCTTTAAGGC	1260
	ATGTGTAGTT CATTTTATAT GGTGTGAAAT AGTTCTTATT CATTTATTCA ACACATATTG	1320
50	GTGGAGTGCC TGCTGATGGT AGTACTCTTC AGAGTACTTT GTATATATTT GTGAACACAT	1380
	ATTCTTGCCC TGGAAGCTTA TGTGTCTNTT CAAGGTAGAT CCONTACTCGG TTTCCACCTG	1440
	TTTTCTTCAG CCTCAGGAT GAATTCACCA ATTTACACA TAGCACCAGT TAAGGAATAG	1500
55	GCTTTATTGG AGAAAAGGAA GCCTTATTAG ACCAGCATCA GCAAAAAAAA A	1551

60 (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

10 ACAGAGTCCT CAACAGAACC TAATCATGCT GGCACCCCTAA TTTCTACTTT TTAGGCTGCA 60  
 GAACTGAGAG AACATAAACT CCACTTGTGT AAGCTACCCA GCTATGGTA TTGTTATTA 120  
 TAGCCCCAAGC TAAGTCAGGT GGAAGGGCAG AATATTTTTC AAGAGATCA TTTCTACAA 180  
 15 AACAGAGTTG TTCTAAATGA AATGGCCAGA TATTTCATCT TTTCTACTCT AGTATTATG 240  
 AAAGTTTCAT TAAACACCAC TTGGCCAGCA CCCAGCCCTG CCACTTTCTG AACGGCAAC 300  
 20 AAAAGCAAAT GATTTGAGGA ACAAAGAGT GGACACAGAG CTTCTCAGAA CATGGCTCA 360  
 TCTTCTGAGA TGATCTTCTG AGATCATCAA TTTTCTGAC CTAAGTCTCT ACTCCAATTG 420  
 TAGTAGATAA GAGCAAAGAC ACTTCCTGAT CCGTCTGAAA ATGCTGGAGC CCGTCTGATG 480  
 25 GAGAGGCTGA CACTGGGACC AACAGAAGGC CGGACATTA TTGTTCTGAG CCTTCTCTGA 540  
 CCTGGGCCCT CTTGAGGCCT TGTACCTTGC ACTCCCATG CCACTGTAGC AACTGCTAAG 600  
 30 CTGAAGTTAG GTATTGGAAG AGATAATTTC CCCCCAACA AATATACTT AAAGAAAAA 660  
 GGAAACCACT AAATTCCACT TGACAAACCA GTTGTCTGAG TTTTACTTT TGCAAATTG 720  
 35 AAAGTTCTC TTTGGCACCA TATGATTCTG TTACATAGG GTTCTCATG CTAAGATAC 780  
 ACAGCTAGGT CTACCAGCTG CCACTGGTCA AGATGAAA AGCTTCTGAG AGAGGATCA 840  
 GTTTCTAATA ACCTAACAGT TTTCCTTGGT TATTACAAA AAAAAAAA TTAGAATAA 900  
 40 ATGTCAGTGC CATGCAGGCA ACTACAGATA TGGAAATGA AGCTTCTGCT ACAACTGCA 960  
 GATTGTGTTG TTAATAAAAT TGATTGGGAT CACTCGA 997

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

GAATTCGGCA CGAGTGACCA CAGATATCTT TGGCTTTCTG CCTCAGGAGA ATGCTGTCCA 60  
 CTATGTTTTT TTAATCGAT TGACATCTCA TGAATCCAGA AATTAGCCG CTTTTCATC 120



467

TTTTCCATCT TTGTCATAGC TTCATCACGC ACGATGGAGG TCACTTCAGC ACTATCCGGA 130  
 GCGGCTCAGC GGACAGATCT GTGAATTTCC TTTTCCTTTT TCTTGATGTA CCGGATTGTC 240  
 5 GACTCGTTTA CATTGAGCTC ATGGCCAACA GCACTGTAAC TCATGCCTGA TTGGAGCTTA 300  
 TCCAACACGC GGAMTTTCTC CGTAAGGSAM ATCAMGGTCT TCTTTCGCTT AGGAACACTG 360  
 10 GGCARARCTT AARCACTACG CTTGGGGGCC ATTTTAGAAA GCAAAACCAC CCACAAAAG 420  
 CAGAAAAAAA AGTGTCACTA AACACACTGN NGANAGGACT CTTTGTTTAC AGCAGAGGAG 480  
 CTGCGACTAG AAGGCGGGCC TTCTCCCCAG TTCAAACTTC AGCTGGGAAC CTTACCTCCG 540  
 15 CCAACTCCAA ATTTTCACCC TCTGCGCATG CCGGGGAAAS AAACCCCGAG AACAGTACCG 600  
 TGATGATTGA TTTTAGGGTT ACAATACAT TTTAGCAAGT AAGTGAATTT GGCATTACGA 660  
 20 ATTAATGATT AATGAAGGTC ACCTGTATTT CCATAGATAT GTAATTTTAT TTAAGCAGGT 720  
 TTATTATATT AAGGCGGSGA GGCAGCGCCG AAGACTACAA GTTCCAGCAT GCACCGCGTC 780  
 CCGGCGGGTT CCGGCTCCCA GCGAGGCTT CAGGACGCC AGCCCGGAGG CATCGGCGCG 840  
 25 AAGTGTCTA GCGCAACCAC GTAGTACTCT CTGCGCATGT GCAAGCGCT GTGGGGGCCC 900  
 GCCCTAGCTG CCGTCGCGCG CCGCGGGGCT CTATGGTCTC TCCCTAGAGC TTGCGCTTG 960  
 GAGGCGGCTG CTGCGGTCTT GTGAGTTTGA CCAGCTCGA GCGGCAGCA CATGGAGGAA 1020  
 30 TTGACTCCG AAGACTTCTC TACGTCGGAG GAGGACGAG ACTACGTGCC GTGGGTGAG 1080  
 CGATTCCGCC TGAGGCGAGA AGCGAATTGC CCGCCCCAC GCTCACGTG AGGCGCGCTC 1140  
 35 TGCCCCCGCG GCGCTCTGCC CTGTGCCCCA GGTGTCCAG GGGGGCTCT GTTCTCGAGC 1200  
 GTCCGCTCCC TCAGGCCCCT CATCTCGGC CGCTCCGCC CGAGGCGTGT GCGGTGCGC 1260  
 GTTCTGTGCT CCCCTCCCT TGGCAGCTC CGCGCGCGC CCCCTCTTC AGCGCGGAA 1320  
 40 CCGCAGATGG ACACGCCCC TTGTGCTAG GGAGCTCTT CGGTACGCC CGAACGACAA 1380  
 CGCTGCTTCA GAAGTCGGG CGCAGTTTG AGCCTTGGAA GTTTTTTCA GCGCTGGGCC 1440  
 45 GAGAGAGCTG CTGGCCAACA ACCCGTCCAA GATAGAGCTG TCCGNTCTCC GNTTGG 1496

50 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

60 TTGCCAGCNG GGAGAGGAA AGAGGAGGAA ATGGGTTTG AGGACCTGG CTTACCTTTC

50

CTGCCCTTTGA CCCATCACAC CCCATTTCCT CCTCTTTCCC TCTCCCGCT GCCAAAAAA 120  
 AAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG 180  
 5 TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA 240  
 ACACAAACAC TGTCTTTTG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC 300  
 10 GTATTCCACG TTTTATAGCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT 360  
 TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG 420  
 AACCTAGGTA TATCCTTTGG TCTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA 480  
 15 AAAAGCCAGG TATAATGTAA CTCACCCCA GCCTTTGTAC TAAGCTCTTG ATAGTGGATA 540  
 TACTCTTTTA ACTTTAGCCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCC 600  
 20 CATTTTACT ATTAAGAAGA CCAGTGATAA TTTAATTAATG CCACCAACTC TGGCTTAGTT 660  
 AAGTGAGAGT GTGAAGTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC 720  
 AGGCCTTATG TTAATAATCAT GCCTTGAAA AGCAAACCTT AATCTGCAA GACAGCAGCA 780  
 25 AGCATTATAC GGTCACTCTG AATGATCCCT TTGAAATTTT TTTTGTGTT GTTTGTTTAA 840  
 ATCAAGCCTG ACGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTT TGTGAATGCT 900  
 30 AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC 960  
 TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAACT GTTTACATTC ATTATGGGGT 1020  
 ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA 1080  
 35 ATGTCAGAAT GGAAGTCTC CTCGAAGTTC TCCCAAATC AGAGACAGCA CTGCCTTCTC 1140  
 CTAAATGATT ATTCTTTTCT CCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA 1200  
 40 GCCATAACCC TTTTACTT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTGGGTATA 1260  
 TAATACTGGT WCCAACAMAG GGGTCTGGA TGTACACMAG GTTATCTT 1308

## (2) INFORMATION FOR SEQ ID NO: 216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1705 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

TGGCCATGGA AGCGCTAGAA GGTTAGATT TTGAAACAGC AAAGAAGGAT TTCCTTGGAT 60  
 CTGGAGACCC CAAAGAAACA AAGATGCTAA TCACCAACA GGCTGACTGG GCCAGAAATA 120

	TCAAGGAGCC CAAAGCCGCC GTGGAGATGT ACATCTCAGC AGGAGAGCAC GTCAGGCGCA	180
	TGGAGATCTG TGGTGACCAT GGCTGGGTG ACATGTTGAT CGACATCGCC CGCAAACTGG	240
5	ACRAGGCTGA GCGCGAGCCC CTGCTGCTGT GCGCTACCTA CCTCAGAGAG CTGGACAGCC	300
	CTGGCTATGC TGCTGAGACC TACCTGAAGA TGGGTGACCT CAAGTCCCTG GTGCAGCTGC	360
10	AGTGGAGACC CAGCGCTGGG ATGAGGCCTT TGCTTTGGCT GAGAAGCATC CTGAGTTTAA	420
	GGATGACATC TACATGCCGT ATGCTCAGTG GCTAGCAGAG AACGATCGCT TTGAGGAAGC	480
	CCAGAAAGCG TTCCACAAGG CTGGGCGACA GAGAGAAGCG GTCCAGGTGC TGGAGCAGCT	540
15	CACAAACAAT GCCGTGGCGG AGAGCAGGTT TAATGATGCT GCCTATTATT ACTGGATGCT	600
	GTCCATGCAG TGCCCTCGATA TAGCTCAAGA TCCTGCCCGAG AAGGACACAA TGCTTGGCAA	660
20	GTCTACCCAC TTCCAGCGTT TGGCAGAGCT GTACCATGGT TACCATGCCA TCCATCGCCA	720
	CACGGAAGAT CCGTTTCAGTG TCCATCGTCC TGAAACTCTT TTCAACATCT CCAGGTTTCT	780
	GCTGCACAGC CTGCCCAAGG ACACCCCTC GGGCATCTCT AAAGTGAAAA TACTCTTCAC	840
25	CTTGGCCAG CAGAGCAAGG CCCTCGGTGC CTACAGGCTG GCGCGGCAGG CCTATGACAA	900
	GCTGCGTGGC CTGTACATCC CTGCCAGATT CCAAAAGTCC ATTGAGCTGG GTACCCCTGAC	960
30	CATCCGCGCC AAGCCCTTCC ACGACAGTGA GGAGTTGGTG CCCTTGTGCT ACCCCTGCTC	1020
	CACCAACAAC CCGCTGCTCA ACAACCTGGG CACGCTCTGC ATCAACTGCC GCCAGCCCTT	1080
	CATCTTCTCC GCCTCTTCT ACGACGTGCT ACACCTGCTT GAGTTCTACC TGGAGGAAGG	1140
35	GATCACTGAT GAAGAAGCCA TCTCCCTCAT CGACCTGGAG GTGCTGAGAC CCAAGCGGGA	1200
	TGACAGACAG CTAGAGATTT GCAACAACA GCTCCAGAT TCTTGGGGCT AGTGGGAGAC	1260
40	CAACGGACTC CATCGGAGAT NAGGACCCGT TCACAGCTAA GCTRAGCTTT GAGCAAGGTG	1320
	GCTCARAGTT CGTGCCAGTG GTGGTGAGCC GGCTGGTGT GCGCTCCATG AGCCGCGGG	1380
	ATGTCTCAT CAAGCGATGG CCCCCACCCC TGAGGTGGCA ATACTTCCGC TCACTGCTGC	1440
45	CTGACGCCCTC CATTAACATG TGCCCCCTCT GCTTCCAGAT GTTCCATTCT GAGGACTATG	1500
	AGTTGCTGGT GCTTCAGCAT GGCTGCTGCC CCTACTGCCG CAGGTGCAAG GATGACCCTG	1560
50	GCCCATGACC AGCATCCTGG GGACGGCCTG CACCCCTGTC CCGCCTTGGG GTCTGCTGGG	1620
	CTGTGAAGGA GAATAAAGAG TTAAGTCTC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1680
	AAAAAAAAA AAAAAAAAAA AANA	1705

55

(2) INFORMATION FOR SEQ ID NO: 217:

60

(1) SEQUENCE CHARACTERISTICS:

470

(A) LENGTH: 999 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

	AGCAAATCAC CTTAACGATC TGAATGAAA CTGTGACCAG TGCCGCCCTG GGTGGTTCTG	60
10	GAGAGACTGC CGTCTTCTTG TTGGCCATA GGTGCTGGG CCCC GGCTTC AGTCACTGTC	120
	TCAGACAGKA GTCCCGATAA GCAGATCACC AGTCTCCAC TGTCTTCCT GTCCGCCTTG	180
15	CTGCATGAGA AGATAGCTGC TTCTCCCTC TTTCTCTAGA CTGTAAATTA TTGTTTACA	240
	ATTGAGTGYC TTAATAATAG TYTACAAATA CTATGTATTT ATGCAAACT GTTAAAGTTC	300
	TCATCTGTTA TGATTGGATA CTGGTCTTG TCAGTAGTGG TCAGCATTGG GTTGTGAGCT	360
20	TGTCCTACTC CATACGTGTT TATCTGCTA TGCATTTTAC ATTGTGTGTT CACATCTATT	420
	CCAAGGAGCC TTCTAGAAA CAACACTGGC GGTCTCTGCA GGCCAGGCAG GCATTGGCCC	480
25	ATGCTGTGTC CCATAGGAGC CAATGGAAAG AACGTAGCTT GGTCTGCTAG CCAGCCGTGG	540
	GGTGGCGCAG GCCAGGCAGC CTCTGCACCA GAGTCCAGCA CCTGCCCATT CCCCAGTCAC	600
	ACRATCATAC TCTTCTTTCA TAGAGATTTT ATTACCACCT AGACCACCCT AGTTTTCCTC	660
30	TCTGTTAGTG TCCTGAGCTC TTTTGCAACA AAATGTAGGT ACAGACCAAT CCCTGTCCCT	720
	TCCCCAATCA GGAGCTCCAC ACCATGAGTT GTTTGTTTTT CCAGAAGCTG CCAGTGGGTT	780
35	CCCGTGAATT GCGTTAAGAT ATCGATGATX TTTTTATTG TTTTCTTCT TGTTTTTTTA	840
	AATAATATAT TTAAGGCAG TATCTTTTGT ACTGTGAATT TGCAGTAGAA GATGCAGAAT	900
	GCACTTTTTT TTTACTTCTG TTGGTGTGTA TTGTATATAG TGTGTGTGCT TCTTGTGATG	960
40	AAAATAAACT TTTTCTTTAT AAAAAAAAAA AAAAAAAC	999

45

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 941 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

55	GGCAGAGTA GCATTTTATT TAATCTGCAG GTATATCTC CCAACAGTTT ATTGTCATGT	60
	GATGTCCTCA GCCAAGATTG TRAGGCAGAG AGGAGCTGTC CCAACCTACT ATACCACCGA	120
60	GGCTGGAGAG ATCATATTTT TGSTATTAAA CTGGAGTCTC TCCATCCTTC ACATTGTTGA	180

471

TGTCTCTGT AGCAAACGGG AAAAGTCAGT CACAGAAGAT GCCGCTACCG GTTTGAGCCA 240  
 GAGAATGACA GCTCTGTTT GGAGAAAAGG CCCGGATGGT GGCTCTAGAA AGCCCATCTT 300  
 5 TCTGCTCTTC TTTTTCTCC CCCTTATATT GTGCTTTCAT TCATTCATTTC ATTTCATCAA 360  
 CATTGTGTGA GCACCTATTA TGTGTCAAGC TCTGTGCTAG CCTCTGGAAA ACCTGCCCTC 420  
 ATGTAGCTCA CTGTGGAGTA GGAGAAACAA TGACTACACT ATGATAAGCA CGGGTTGTCA 480  
 10 GGGTCTCACA GAGCAGTGGC CCCTCATCCA GACCGATGAG GTCAAAGAAG GCATCCAGGC 540  
 GAGGATGGTG TCAGAGCTAA CTGAAGAATG AGAGGGAGCT GCACCAACAG GGGTTGGAAC 600  
 15 TGAAGGTGGC AGTGCCTGGA GTCTTGATTTC CAGCAGAGGG AGAGCAGTCT GTGAAAAGGC 660  
 ACCAAGGGTG GCAGAGGGCA GAGCACATGG AGGAACTTCA GGTAGTTCTG GATGGCCTG 720  
 GGGCAAAGCT AGAGAGGTAA GAAGAATCTA CAATGTCTC TCGAGTTACA TGAACCTCCA 780  
 20 TCCCAATAAA CCCATTGGAA ACGAAAAATT TAAGTCAGAA GTGCATTTAA GGCTGGTCCG 840  
 AGTAGAATGA TTTTACAAC GAATTGATCA CAACCAGTTA CAGATGTCTT TGTTCCTTCT 900  
 25 CCACTCCAC TGCTTCACCT GACTAGCCTT TAAAAAAA A 941

30 (2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 575 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

40 TAAGTGGAAAT CCCCCGGGT TGCAGGAAT TCGGCACGAG GCATCTGAG AAGCTTAAGA 60  
 CATACTTTGA AGACAACCTT AGGACCTCC AGCTGCTGG GCATGACCTA CCTTTGCACC 120  
 CCGCAGTGGT GAAGCCCCAC CTGGGCCATG TTCCTGACTA COTGGTTCCT COTGCTCTCC 180  
 45 GTGGCCTGGT RCGCCCTCAC AAGAAGCGGA AGAAGCTGTC TTCCTCTTGT AGGAAGGCCA 240  
 AGAGAGCAA GTCCAGAAC CCACTGCCA GCTTCAAGCA CAAAGGAAAG AAATTCAGAC 300  
 50 CCACAGCCAA GCCCTCCTGA GGTGTGTGG CCTCTCTGA CTEAGCACA TTGTGGAGCA 360  
 CAGGCTTACA CCTTCGTGG ACAGGCGAGG CTCTGGTCT TACTGCACAG COTGAACAGA 420  
 CAGTCTCTGG GCTGGCAGTG CTGGGCCCTT TAGCTCCTTG GCACTTCCAA GCTGGCATCT 480  
 55 TGCCCCCTGA CAACAGAATA AAAATTTTAG CTGCCCAA AAAAAAAAAA AAAAAAAAAA 540  
 CTCGAGGGGG GGCCCGTACC CAATTCGCCC TATAA 575

60

## (2) INFORMATION FOR SEQ ID NO: 220:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3018 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GCCAGCCTTA CAGCTTTTAC GTGAAATGAA AGCCATTGGA ATAGAACCCT CGCTTGCAAC	60
ATATCACCAT ATTATTGCCC TGTTCGATCA ACCTGGAGAC CCTTTAAAGA GATCATCCTT	120
CATCATTTAT GATATAATGA ATGAATTAAT GGGAAAGAGA TTTTCTCCAA AGGACCCCGA	180
TGATGATAAG TTTTTCAGT CAGCCATGAG CATATGCTCA TCTCTCAGAG ATCTAGAACT	240
TGCCTACCAA GTACATGGCC TTTTAAAAAC CGGAGACAAC TGGAAATTCA TTGGACCTGA	300
TCAACATCGT AATTTCATTT ATTCCAAGTT CTTGGATTGG ATTTGTCTAA TGGAAACAAAT	360
TGATGTTACC TTGAAGTGGT ATGAGGACCT GATACCTTCA GCCTACTTTC CCCACTCCCA	420
AACAATGATA CATCTTCTCC AAGCATTGGA TGTGGCCAAT CGGCTAGAAG TGATTCCTAA	480
AATTTGGGAA AGATAGTAAA GAATATGGTC ATACTTTCCG CAGTGACCTG AGAGAAGAGA	540
TCCTGATGCT CATGGCAAGG GACAAGCACC CACCAGAGCT TCAGGTGGCA TTTGCTGACT	600
GTGCTGCTGA TATCAAATCT GCGTATGAAA GCCAACCCAT CAGACAGACT GCTCAGGATT	660
GGCCAGCCAC CTCTCTCAAC TGTATAGCTA TCCTCTTTTT AAGGGCTGGG AGAACTCAGG	720
AAGCCTGGAA AATGTTGGGG CTTTTCAGGA AGCATAATAA GATTCTCTAG AGTGAGTTGC	780
TGAATGAGCT TATGGACAGT GCAAAAGTGT CTAACAGCCC TTCCCAGGCC ATTGAAGTAG	840
TAGAGCTGGC AAGTGGCTTC AGCTTACCTA TTTGTGAGGG CCTCACCAG AGAGTAATGA	900
GTGATTTTGC AATCAACCAG GAACAAAAGG AAGCCCTAAG TAATCTAACT GCATTGACCA	960
GTGACAGTGA TACTGACAGC AGCAGTGACA GCGACAGTGA CACCAGTGAA GGCAAATGAA	1020
AGTGGAGATT CAGGAGCAGC AATGGTCTCA CCATAGCTGC TGGAAATCACA CCTGAGAACT	1080
GAGATATACC AATATTTAAC ATTGTTACAA AGAAGAAAAG ATACAGATTT GGTGAATTTC	1140
TTACTGTGAG GTACAGTCAG TACACAGCTG ACTTATGTAG ATTTAAGCTG CTAATATGCT	1200
ACTTAACCAT CTATTAAATGC ACCATTAAAG GCTTAGCATT TAAGTAGCAA CATTGCCGTT	1260
TTGAGACACA TGGTGAGGTC CATGGCTCTT GTCATCAGGA TAAGCCTGCA CACCTAGAGT	1320
GTCCGTGAGC TGACCTCAGC ATGCTGTCCT CGTGGGATTG CCCTCTCCTG CTGCTGGACT	1380
TCTGCCTTTG TTGGCTGAT GTGCTGCTGT GATGCTGGTC CTTTATCTTA GGTGTTCTATG	1440

60

	CAGTTCTAAC ACAGTTGGGG TTGGGTCAAT AGTTTCCCAA TTTCAGGATA TTTCGATGTC	1500
	ACAAATAACG CATCTTAGGA ATGACTAAAC AAGATAATGG CAGTTTAGGC TGCACAAC TG	1560
5	GTAAATGAC TGTAGATAAA TGTGTAAAT AGTGTAACG TTTGTATTTT TGTAAATATA	1620
	CCCCGTGCCA TAGTTTTCTA ACTTGAACAG CCATGAATGT TTCAATGCTC CCTTTTTTTT	1680
10	TTGTCTATAG CTGTTACCTA TTTTAGTGGT TGAATGAGA GCTAGTGATG ACAGAAGGAT	1740
	GTGGAATGTC TTCTTGACAT CATTGTGTAT TGCTGCTAAT CAAGTTGCTA ACCACTACTT	1800
	CTAGCAGCTC TTACCACTAT GACTTAAGTG GTCTTGGAG GCAGTAAGTG GAGGTTTGCA	1860
15	GCATTCTGTC CTTTCATGAGG GCTTCTACCA CTGACCACTT TGCACGTACC TGGCTCCAG	1920
	ATTTACTTAG CTACCCACG AGTCCTCCAC ATAAGCAGCT TCATCTTTAC CTTGCCAGAG	1980
20	TTGACAATTA TGGGATACTC TAGTCTACTT ATACTTGTGT TCCCATCTGT CTGCCATCCT	2040
	CTGAAGGCCA GGACCCAGTC ATACATCCTT AGAAACCAAA GTATGGTTTT TGTMTCTCT	2100
	TGGAATGTCA GGTCTTAAGG CATTTAATTG AGGACAAAA AAAAAAAAAA GCCGATATAG	2160
25	TAGCTAGCTA CTTAAGCATC CATGGGTATT GCTCCATATC AAAGCAGATT TCCAGGACAG	2220
	AAAGAGTAAA TTAGCCTTCA GTCTTGGTTT ACAGCTTCCA AGGAGAGCCT TGGSCACCTG	2280
30	AAATGTTAAC TCGGTCCCTT CCTGTCTCTA GTTCATCAGC ACCTGCAGAT GCCTGACTCT	2340
	TGTTAGCCTT ACTATTCAAT ACAGTCCTTA GATTCACGGT ATGCCTCTTC CTATCCAGGC	2400
	ACCTATTCTG AATCACCATG TTGCTCTGCA GCTAGAGTTG ATAGGAGAAA ATCCATTTGG	2460
35	GTAGATGGCC TATGAATTC TAGTAGACTT TCAAAATGAG TGATTTGTTA GCTTGGTACT	2520
	TTTAAGTTTG TGGTACAGAT CCTQCAAACC CATACTCTGA GCAATTAACT GCCTTGAACA	2580
40	TAGAGAAAA TTAAGGCCTC ACAGCATGAG TCTCCATTCT CTGTAAATGC TTATTTTATC	2640
	ATAGTCTTTA GCCTCTAACT ATGAGTAAAA TGTCTCTTTC GGGCGGTGT GGTGACTCAC	2700
	ACCTGTAACC TCAGCACTTT GGGAGGCAGA GGTGGGAGGA TCACCTAGGT CCAGGAGTTC	2760
45	GAGACTAGCC TGGGCAACAT AGTGAGACAC CGGATCTACA AAAAAATAAA AAGCCAGACT	2820
	GGTGGTATGT ATCTGTGTCC CAGCTAATTG GGAGGGTGAG ATGGGAGGAT TGTITGAGCC	2880
50	TAGGAGAGGG AGGTTGCAGT GAGCGTGAT CGCACCAC TG CACTCCAGCC TGGGCAACAG	2940
	AGCAAGACCC TGTCTTGGAG AAACCAGAAT TTTGGAAGAG CAAATGGGGC TGACTGCAGT	3000
55	GGCTCATGCC TGTAAATCC	3018

(2) INFORMATION FOR SEQ ID NO: 221:

60 (i) SEQUENCE CHARACTERISTICS:

474

- (A) LENGTH: 963 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

	GGCAGGAGGG CCGCGGGACA TCCACGGGGC GCGAGTGACA CCGGGGAGGG AGAGCAGTGT	60
10	TCTGCTGGAG CCGATGCCAA AAACCATGCA TTTCTTATTC AGATTTCATTG TTTTCTTTTA	120
	TCTGTGGGGC CTTTTTACTG CTCAGAGACA AAAGAAAGAG GAGAGCACCG AAGAAGTGAA	180
	AATAGAAGTT TTGCATCGTC CAGAAAACCTG CTCTAAGACA AGCAAGAAGG GAGACCTACT	240
15	NAAATGCCCA TTATGACGGC TACCTGGCTA AAGACGGCTC GAAATCTCTAC TGCAGCCCGA	300
	CACAAAATGA AGGCCACCCC AAATGGTTTG TTCTTGGTGT TGGGCAAGTC ATAAAAGGCC	360
20	TAGACATTGC TATGACAGAT ATGTGCCCTG GAGAAAAGCG AAAAGTAGTT ATACCCCTT	420
	CATTGCGATA CGGAAAGGAA GGCTATGCG AGGCAAGAT TCCACCGGAT GCTACATTGA	480
	TTTTTGAGAT TGAACCTTAT GCTGTGACCA AAGGACCACG GAGCATGAG ACATTTAAAC	540
25	AAATAGACAT GGACAATGAC AGGCAGCTCT CTAAAGCCGA GATAAACCTC TACTTGCAAA	600
	GGGAATTTGA AAAAGATGAG AAGCCACGTG ACAAGTCATA TCAGGATGCA GTTTTAGAAG	660
30	ATATTTTTAA GAAGAATGAC CATGATGGTG ATGGCTTCAT TTCTCCCAAG GAATACAATG	720
	TATACCAACA CGATGAACCTA TAGCATATTT GTATTTCTAC TTTTTTTTTT TAGCTATTTA	780
	CTGTACTTTA TGTATWAAAC AAAGTCMCTT TTCTCCMAGT TGKATTTGCT ATTTTTCCCC	840
35	TATGAGAAGA TATTTTGATC TCCCCAATAC ATTGATTTTG GTATAATAAA TGTGAGGCTG	900
	TTTTGCAAC TTAATAAAAA ATTTAAAAAA ACTGGAGGGG GGCCCGTACC CAANTCGCCG	960
40	NATATGAT	963

45

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

55	CGTTTTCCGG CCGTGGGTTT GTGGCCGTCC GGCCTCCCTG ACATGCAGCC CTCTGGACCC	60
	CGAGGTGGA CCCTACTGTG ACACACCTAC CATGGGACA CTCTTCAACC TCCTCTGGCT	120
60	TGGCCTGGCC TGCAGCCCTG TTCACACTAC CCTGTCAAG TCAGATGCCA AAAAGCGGC	180



CTCAAAGACG CTGCTGGAGA AGAGTCAGTT TTCAGATAAG CCGGTGCAAG ACCGGGGTTT 240  
 GGTGGTGAGG GACCTCAAAG CTGAGAGTGT GGTTCCTTGAG CATCGCAGCT ACTGCTCGGC 300  
 5 AAAGGCCCCG GACAGACACT TTGCTGGGGA TGTACTGGGC TATGTCACCT CATGGAACAG 360  
 CCATGGCTAC GATGTCACCA AGGTCTTTGG GAGCAAGTTC ACACAGATCT CACCCGTCTG 420  
 GCTGCAGCTG AAGAGACGTG GCCGTGAGAT GTTTGAGGTC ACCGGCCTCC ACCAGCTGGA 480  
 10 CCAAGGGTGG ATGCGAGCTG TCAGGAAGCA TGCCAAGGGC CTGCACATAG TGCTCGGCT 540  
 CCTGTTTGAG GACTGGACTT ACGATGATTT CCGGAACGTC TTAGACAGTG AGGATCAGAT 600  
 15 AGAGGAGCTG AGCAAGACCG TGGTCCAGGT GGCAAAGAAC CAGCATTTGG ATGGCTTCGT 660  
 GGTGGAGGTC TGGAAACCAGC TGCTAAGCCA GAAGCCCGTG GGCCTCATCC ACATGCTCAC 720  
 CCACTTGGCC GAGGCTCTGC ACCAGGCCCG GCTGCTGGCC CTCCTGGTCA TCCCGCTGC 780  
 20 CATCACCCCC GGGACCGACC AGCTGGCCAT GTTCACGCAC AAGGAGTTTG AGCAGCTGGC 840  
 CCCCCTGCTG GATGGTTTCA GCCTCATGAC CTACGACTAC TCTACAGCGC ATCAGCCTGG 900  
 25 CCCTAATGCA CCCCTGCTCT GGGTTGAGC CTGCGTCCAG GTCTGGACC CGAAGTCCAA 960  
 GTGGCGAAGC AAAATCCTCC TGGGGCTCAA CTCTATGGT ATGGACTACG CGACCTCCAA 1020  
 GGATGCCCCG GAGCCTGTTG TCGGGGCCAG GTACATCCAG ACACTGAAGG ACCACAGGCC 1080  
 30 CCGGATGGTG TGGGACAGCC AGGYCTCAGA GCACTTCTTC GAGTACAAGA AGAGCCGCAG 1140  
 TGGGAGGCAC GTCGTCTTCT ACCCAACCCT GAAGTCCCTG CAGGTGCGGC TGGAGCTGGC 1200  
 35 CCGGGAGCTG GCGGTGGGG TCTCTATCTG GGAGCTGGCC ACGGCCTGGA CTACTTCTAC 1260  
 GACCTGCTCT AGGTGGGCAT TCGGGCCTCC GCGGTGGACG TGTTCTTTTC TAAGCCATGG 1320  
 40 AGTGAGTGAG CAGGTGTGAA ATACAGGCCT NCACTCCGTT TGCTGTGAA AAAAAAAAAA 1380  
 AAAAAAAAAA AAAAAAAAAA AAAA 1404

45

(2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 707 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

55

NGCGCGCCTG CAGTCGACAC TAGTGGATCC AAAGAATTCG GCACGAGGGC AGGTCCAGGG 60  
 CTCAGAAATC AGCTCTATTG ACCAATTCG CCGCAAGTTC CGCCTGGACT GCGCGCTGGC 120  
 60 CATGGAGCTG ATCAAGGAGG ACCGGCCCAT CACCATCAAG GACGACAAGG GCAACCTCAA 180

CCGCTGCATC GCAGACGTGG TCTCGCTCTT CATCACGGTC ATGGACAAAC TGGGCTTGA 240  
 GATCCCGCGCC ATGGATGAGA TCCAGCCCGA CTTGCGAGAG CTGAGGGA GAATGCAACG 300  
 CATGAGCCAC CTCCACCCCG ACTTTGAGGG CCGCGACAGC GTGAGGCACT GGTTCAGAC 360  
 CTTGAGCGGC ATGTGGGCGT CAGATGAGCT GCGCACTCA CAGGTGCTTC AGATGCTGTT 420  
 CGACCTGGAG TCAGGCTACA ACCGCTTCAA CCGCTTCTG CATGCTGAG CTTGGGGCAC 480  
 TAGCCCTTGC ACAGAAGCGC AGAGTCTGAG CGATGCGTC CTGCTGCTCT GTCCGCCACA 540  
 CAGGCGGTGG TCATCCACAC AACTCACTGT CTGAGGTGC CTGTCTGTC TCTGCTTTG 600  
 GTGTGAGAAC TTTTGGGCGG GGGCGCTCCC CCAATTAAG ATGCTCTTGG ACCTTCAAAA 660  
 AAAAAAAAAA AAAAAGCTCG GGGGGGCGCG GTCCCAATCC CCGCTCT 707

## (2) INFORMATION FOR SEQ ID NO: 224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GGGGAAGTGC AGTGACAGCA GGAATAGAG TGGAGGCGAG GATAGAGTG GGCACAGGT 60  
 ATGGAGAGGG GGTTCAGCGA GCCTAGAGAG GCGAGATAT CAGGGTGCTG GCGGTGAGAA 120  
 TCCAGGGAGA GGAGCGAAA CAGAGAGGG GAGAGAGACC GGGGCTTTC TGGTTGCAG 180  
 AGCCCTCTAG CCATGTTGGG AGCAGAGCA CATGCGTAC CAGGTCTTCT AAGAGTCCC 240  
 GGGCTGCCCT TGGTTCTGCT GTTCTGCGC CTGGGGGCGG GTTGGGCTCA GGAGGGGTCA 300  
 GAGCCCGTCC TGCTGGAGGG GAGTGGCTG GTGGTCTGT AGCTGGGCG AGTGTCTGCA 360  
 GGGGGGCGCG GGGAGGAGC CTTGGGAGAG GCACCCCTG GCGAGTGGC ATTTGCTGG 420  
 GTCCGAAGCC AACACCATGA GCGAGAGGG GAAACCGCA ATGGCACTK TGGGCGATC 480  
 TACTTCGACC AGTCTCTGCT GAACGAGGGC GTTGGCTTTG ACCGGGCTTC TGGTCTCTC 540  
 GTAGCCCTCT TCCGGGCTGT CTACAGCTTC CCGTTCTATG TGTGAGGT GTACACCGC 600  
 CAAACTGTCC AGGTGAGCT GATGCTGAC AGTGGGCTG TCATCTGAGC CTTTGCCAAT 660  
 GATCTGACG TGACCCGGA GGCAGCCACC AGCTCTGTG TACTGCTTT GAGCTCTGG 720  
 GACCGAGTGT CTCTGCGCT GCGTGGGGG AATCTCTGG GTGTTTGA AATCTCAAGT 780  
 TTCTCTGGCT TCCTCATCTT CCGTCTCTGA GACCCAGT YTTTCAAGCA CAGATCCA 840

477

GCCCCGACA ACTTTCTCTT GGCCTCTCTT GCCCCAGAAA CAGCAGAGGC AGGAGAGAGA 900  
 CTCCCTCTGG YTCCTATCCC ACYTCTTTGC ATGGGAMCCT GTGCCAACA CCCAAGTTTA 960  
 5 AGAAAAARY ARARCTGWWG CAGGTATACA GAGCTGGAAG TGGACCATGG AAAACATSCA 1020  
 TAACCATGCA TCYTCTTGCT TGGCCACCTC CTGAAACTGT CCACCTTTGA AGTTTGAAC 1080  
 TTAGTCCCTC CAMACTCTGA CTGCTGCCCTC CTTCCTCCCA GCTCTCTCAC TGAGTTATYT 1140  
 10 TCACTGTACC TGTTCAGCA TATCCCACT ATCTCTCTTT CTCTGTATCT GTGCTGTCTT 1200  
 ATTCTCTCC TTAGGCTCC TATTACCTGG GATTCCATGA TTCATTCCTT CAGACCTCT 1260  
 15 CCTGCCAGTA TGCTAAACCC TCCCTCTCTC TTTCTTATCC CGCTGTCCCA TTGGCCACG 1320  
 CTGGATGAAT CTATCAATAA AACAACTAGA GAATGGTGGT CAAAAAAAAA AAAAAAAAAA 1380  
 TCGA 1384  
 20

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 760 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GGGTCGACCC ACGCGTCCGC TGACCAGTCC GTTATAGATA CTTCTTCCTA TACCAAACT 60  
 35 GTTTAAACAG GTGCCACCAC AAGGGATGTC GTCCTTACTC TCTGCGGGTC TTCAAGCATC 120  
 CCTTTGTGGG AAAGTCTCT GGGCAAGCAC GTGGTATTG GTCTGCTGCT TGCTTCCCTT 180  
 40 TTCCACCAG GGATGTTGTG ATCATAAGTC AAAACACAG TATATTCCAA ATCTCAAAG 240  
 CTATTGTGGC CTGAGCACA TTGAAATCTA GCAGAGTTTT TCCTATGTAG CTTTAGAGTA 300  
 ACTCTTCTGC TTCTCTGTCA CTTACAATTC AGGTTCTGCC TTTGCCTAAG AGCATGAGCA 360  
 45 GAAGAGTCTT CATGTGACGC TTAGTTCTAT TGCAGTCTG GGTGAAACTA TTAAAGCAT 420  
 GGGGCTGCTK CTCCCCANWT CCTCCCTAAC AATTCGTGT GTGGACTTCT CATCTAAAAG 480  
 50 GTTAGTGGCT TTTGCTTGGG ATCAGTGCTC TCTATTGATG TTCTTGCTGG TCTCCAGACA 540  
 CATTCCTGTT GCATTAGAC TTGAAAGACT TGTAGATGTG TGATGTTGAG GCACAGGATG 600  
 CTGAAAGCTA TGTTACTATT CTTAGTTGT AAATTGTCTT TTGATACCA TCATCTTGT 660  
 55 TTCTTTTGT AGGTATAAAT AAAAACA CTG TTGACAATAA AAAAAAAAAA AAAAAAAAAA 720  
 AAAAAAAAAA AAAAAAAAAA NAAAAAAAAA AAAAAAAAAA 760

60

## (2) INFORMATION FOR SEQ ID NO: 226:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2057 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

CCGAGCCGGC TGGCGCGGGG GAATCCGTGC GGGCGCCTTC CGTCCCRGTC CCATCCTGGC 60  
CGGCCTCCAG CACCTCTGAA GTTTTGCAGC GCCCAGAAAG GAGGCGAGGA AGGAGGGAGT 120  
GTGTGAGAGG AGGGAGCAAA AAGCTCACCC TAAAACATTT ATTTCAAGGA GAAAAGAAAA 180  
AGGGGGGGCG CAAAATGGC TGGGGCAATT ATAGAAAACA TGAGCACCAA GAAGCTGTGC 240  
ATTGTTGGTG GGATCTGCT CGTGTTCCTT ATCATCGCCT TTCTGGTGGG AGGCTTGATT 300  
GCTCCAGGGC CCACAACGGC AGTGTCTTAC ATGTGGGTGA AATGTGTGGA TGCCCGTAAG 360  
AACCATCACA AGACAAAATG GTTCGTGCTT TGGGGACCCA ATCATTGTGA CAAGATCCGA 420  
GACATTGAAG AGGCAATTCC AAGGGAAATT GAAGCCAATG ACATCGTGTT TTCTGTTTAC 480  
ATTCCCCTCC CCCACATGGA GATGAGTCTT TGGTTCCAAT TCATGTTGTT TATCCTGCAG 540  
CTGGACATTG CTTTCAAGCT AAACAACCAA ATCAGRGAAA ATGCAGAAGT CTCCATGGAC 600  
GTTTCCCTGG CTTACCGTGA TGACCGTTT GCTGAGTGGA CTGAAATGGC CCATGAAAGA 660  
GTACCACGGA AACTCAAATG CACCTTCACA TCTCCAAGA CTCCAGAGCA TGGAGGGCCG 720  
GTTACTATGA ATGTGATGTC CTTCCTTTCA TGGAAATTGG GTCTGTGGCC CATGAAGTTT 780  
TACCTTTTAA ACATCCGGCT GCCTGTGAAT GAGAAGAAGA AAATCAATGT GCGAATTGGG 840  
GAGATAAAGG ATATCCGGTT GGTGGGGATC CACCAAAATG GAGGCTTCAC CAAGGTGTGG 900  
TTTGCCATGA AGACCTTCCT TACGCCCAGC ATCTTCATCA TTATGGTGTG GTATTGGAGG 960  
AGGATCACCA TGATGTCCCG ACCCCCAGTG CTTCTGGAAA AAGTCATCTT TGCCCTTGGG 1020  
ATTTCCATGA CTTTATCAA TATCCAGTG GAATGGTTTT CCATCGGGTT TGAATGGACC 1080  
TGGATGCTGC TGTGTTGTGA CATCCGACAC GCATCTTCTA TGCRATGCTT CTXTCCTTCT 1140  
GGATCATCTT CTGTGGCGAG CACATGATGG ATCAGCACGA GCGGAACCAC ATCGCAGGGT 1200  
ATTGGAAGCA AGTCGGACCC ATTGCCGTTG GTCCCTTCTG CTCTTCATAT TTGACATGTG 1260  
TGAGAGAGGG GTACAACCTA CGAATCCCTT CTACAGTATC TGGACTACAG ACATGCGGAA 1320  
CAGAGCTGGC CATGGCTTTC ATCATCGTGG CTGGAATCTG CCTCTGCCTC TAACTTCCTG 1380  
TTTCTATGCT TCATGGTATT TCAGGTGTTT CGGAACATCA GTGGGAAGCA GTCCAGCCTG 1440

CCAGCTATGA GGAATGCGG GGGCTAGAG TATGAGGGG TAATTTTATG GTTCAAGTTC 1500  
 CTCAGGCTTA TCGCTTGGG TCGCTTGGG ATGCTTCTCA TCTTCTTCAT CGTTAGTCAG 1560  
 5 GTACGGGAG GCGATGGGA ATGGGGGGG CCGTACGCTC CCAAGTGAAC AGTGCCTTTT 1620  
 TCGAGGGAT CCGGGGATG TCGATCTGT AGCTTTTGG TGTGATGTC TTGTATGCAC 1680  
 10 CATCCGATAA AACTATGGA GAGGCGCAT CCAATGGAT GCACTCCCA TGTAATCGA 1740  
 GGGAGATTC TCGTTGTTT GTTCGGGAC TTATCGAGA ACTGTTGAGC GCTTCGAAAT 1800  
 ATTCCTTCAAT CATGAGGAG TCGCTTCTG GTATTGAGT CACAAAGGCA ACACATGTTT 1860  
 15 ATCAGCTTTC CATTCGAT TCGAGCTC ACATTGATTC TACTTGATA CGCACACAAA 1920  
 TACACTGAT TACCTTTAT TCGAAATTT TAATATGAG GAAAAAGCG TCAACAATA 1980  
 20 ATATCTTTC ATATCTGCT TACTCTCTT AAAAAAAAA AAAAAACTC GTGCGGAATT 2040  
 CCGCAGGAGC GGCACGA 2057

25

(2) INFORMATION FOR SEQ ID NO: 227:

30

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(2) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

40

45

50

55

60

GCGAGAGGG CATTCCTGC AAGAGGCCAA ACCCGCATTC CTCTGTGCCC CTCCTCTCCC 60  
 ACCGAGTGT TCGAAAAAT ACTCTGTTT ACCGGAATA ACTGTTGATT TTTCACCTCT 120  
 CCTCTGAGG TCGACTTTT CAGAAAAA ATTTGCAAG TGGAAACCG AAGAAAAATA 180  
 TCGAGGGGG AATGAGCTG TCACTGTGT CCGCTCTTC GCTGAGTGTG TGGAGTCTG 240  
 CTGAGGTGT ATGACAGTG TGTGTGAGG TGGTGGTTG AGGGAACCG CTGTTTCAGA 300  
 45 GCTGTGACTG CCGCTGCAAT GCGAGAAAC TGGCTTTGG TGGCTGTAGC GCGGGGCTT 360  
 CTCTCTGCT CAGCATCCAG AAGAGCCAT GTCCGGGAG CAGAAGGTAC CCGGSCAGCT 420  
 50 ACTGGAGGAG TGTGGGGGC TCGCTGGGT GCGGCTCCG CCGTGGGGC CTGTTGCTGC 480  
 TGTCCATTA TTTCTACTAC TCGTCCCAA ATGCGGTGG CCGGCGCTC ACTTGGATGC 540  
 TTGCGCTGCT GGGCTTTTC GAGGGCACTG AACATCTTC TGGGCTCAA GGGCTTGGC 600  
 CCGCTGAGA TCTGTGCAAT GTGTGAATA GGAATTTCA ACTGCGCCA TGGGCTGGCA 660  
 TGTGATATT AGTGGGATA TGTGGGTTG ATCTGCGAG AGCTCCAGG CCGGATTGCA 720  
 60 ACTTACGAT AGATATCAA CAGCTGCTA CCGGTGCG TCGCCAGCG GTGTNATATT 780

	CTCTTCCCAT TGGACTGTGG GGTGCCTGAT AACCTGAGTA TGGCTGACCC CAACATTCCG	840
5	TTCTTGATA AACTGCCCCA GCAGACCGGT GACCGTGCTG GCATCAAGGA TCGGGTTTAC	900
	AGCAACAGCA TCTATGAGCT TCTGGAGAAC GGGCAGCGGG CGGGCACCTG TGTCTTGGAG	960
	TACGCCACCC CCTTGCAGAC TTGTTTTGCC ATGTCACAAT ACAGTCAAGC TGGCTTTAGC	1020
10	GGGGAGGATA GCCTTGAGCA GGCCAAACTC TTCTGCCGGA CACTTGAGGA CATCTTGGCA	1080
	GATGCCCCTG ACTCTCAGAA CAACTGCCGC CTCATTGCCT ACCAGGAACC TGCAGATGAC	1140
15	AGCAGCTTCT CGCTGTCCCA GGAGGTTCTC CGGCACCTGC GGCAGGAGGA AAAGGAAGAG	1200
	GTTACTGTGG GCAGCTTGAA GACCTCAGCG GTGCCCAGTA CCTCCACGAT GTCCCAAGAG	1260
	CCTGAGCTCC TCATCAGTGG AATGGAAAAG CGCCTCCCTC TCCGCACGGA TTTCTCTTGA	1320
20	GACCCAGGGT CACCAGGCCA GAGCCTCCAG TGGTCTCCAA GCCTCTGGAC TGGGGGCTCT	1380
	CTTCAGTGGG TGAATGTCCA GCAGAGCTAT TTCCTCCAC AGGGGGCCTT GCAGGGAAGG	1440
25	GTCCAGGACT TGACATCTTA AGATGCGTCT TGTCCCCTTG GGCAGTCAT TTCCCCTCTC	1500
	TGAGCCTCGG TGTCTTCAAC CTGTGAAATG GGATCATAAT CACTGCCTTA CCTCCCTCAC	1560
	GGTTGTTGTG AGGACTGAGT GTGTGGAAGT TTTTCATAAA CTTTGGATGC TAGTGTACTT	1620
30	AGGGGGTGTG CCAGGTGTCT TTCATGGGGC CTTCAGACC CACTCCCCAC CCTTCTCCCC	1680
	TTCTTTTGCC CGGGGACGCC GAACTCTCTC AATGGTATCA ACAGGCTCCT TCGCCCTCTG	1740
35	GCTCCTGGTC ATGTTCCATT ATTGGGGAGC CCCAGCAGAA GAATGGAGAG GAGGAGGAGG	1800
	CTGAGTTTGG GGTATTGAAT CCCCCGGCTC CCACCTGCA GCATCAAGGT TGCTATGGAC	1860
	TCTCTGCCC GGCAACTCTT GCGTAATCAT GACTATCTCT AGGATCTCTG CACCACTTCC	1920
40	TTCCCTGGCC CCTTAAGCCT AGCTGTGTAT CGGCACCCCC ACCCCACTAG AGTACTCCCT	1980
	CTCACTTGGG GTTTCCTTAT ACTCCACCCC TTTCTCAACG GTCCTTTTTT AAAGCACATC	2040
45	TCAGATTAAA AAAAAAAAAA AAAAAAAAAA AGGGGGGGCN GONT	2084

## (2) INFORMATION FOR SEQ ID NO: 228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TGCACCCACG CCGCGGTTG AATTCCTTGA CTTGCAACA CATATTTATT AGCCTGACTC

60

60

	AAACAATGAA GCTATTAAAA CTTGGGAGGA ACATTGTAAA ACTCTCTTTG TATGGGCATT	120
	TCACCAACAC GCTTATTTTG GCAGTGGCAG CATCCATTGT GTTATCATC TGGACAACCA	130
5	TGAAGTTCAG AATAGTGACA TGTCAGTCGG ACTGGCGGGA GCTGTGGGTA GACGATGCCA	240
	TCTGGCGCTT GCTGTCTCC ATGATCCTCT TTGTCATCAT GGTCTCTGG CGACCATCTG	300
10	CAAACAACCA GAGGTTTGCC TTTTCACCAT TGTCTGAGGA AGAGGAGGAG GATGAACAAA	360
	AGGAGCCTAT GCTGAAAGAA AGCTTTGAAG GAATGAAAAT GAGAAGTACC AAACAAGAAC	420
	CCATGGGAA TGTAAAGTT AACAAAGCAC AGGAAGATGA TTTGAAGTGG GTAGAAGAGA	480
15	ATGTTCCCTC TTCTGTGACA GATGTAGCAC TTCCAGCCCT TCTGGATTCA GATGAGGAAC	540
	GAATGATCAC ACACTTTGAA AGGTCCAAAA TGGAGTAAGG AATGGGAAGA TTTGCAGTTA	600
20	AAGATGGCTA CCATCAGGGA AGAGATCAGC ATCTGTGTCA GTCTTCTGTA CGGCTCCATG	660
	GGATTAAAGG AAGCAATGAC ATCCTGATCT GTTCCTTGAT CTTTGGGCAT TGGAGTTGGC	720
	GAGAGGTGTC AGAACAAAGA GAACATCTTA CTGAAAACAA GTTCATAAGA TGAGAAAAAT	780
25	CTACGAGCTT CTTATTTACA ACACTGCTGC CCCCTTTCTT CCCAGACTCT GACATGGATG	840
	TTCATGCAAC TTAAGTGTGT TGTTCCTGAA CTTTCTGTAA TGTTCATTT TTTAAATCTG	900
30	ACAAACTAAA AAGTTTAAAG TCTTCTAAAA GATTGTCTC AACACCATAA TATGTAATCT	960
	CCAGGAGCAA CTGCCTGTAA TTTTATTTA TTTAGGGAGT TACATAGGTG ATGGGGGAAA	1020
	TTGTTAACTA CCTTTCATTT TCCTGGGAAG TCAAGGTAC ATCTTGCAGA GGTGTTTTTG	1080
35	AGAAAAAAGG GCCCTTCTGA GTTAAGGAGC CATACTTCTA TCAATGATCA AAAGAAAAAA	1140
	AAAAAAAGA GAACTGTTA CAGTATGATT CAGATCATTT AAAAAAGCAA AATCAAGTGC	1200
40	AATTTTGTIT ACAATGGTG TATATTAAAG ATTTTCTAT TTCAGATGTA CTTTAAAGAG	1260
	AAATATTAGC TTAACCTCTT TGACATCTGC TATTGTGACA CATCCCATG CTGGCAATGT	1320
	GGTGCACT CCGAACTTT TAACTACTGT TTTGTAAGCC TCCAAGGCTG GCATTGCAGG	1380
45	GTCTTAGGC AATGTTTTGT TTGCCTTAT GCAGAGAGGT GCTCCAAGTG CTGTGATTGA	1440
	GCACCGTGT AGAGGAAGT TAATGCTTCA GAAGTTGTAG CTTATACAAA GGAAACAGGT	1500
50	CCTGCTGGCT TAATTTAAAC AGTTATGCA TGAAGTAGCG TGGAGGCCCT GGACTGCTGC	1560
	TCGTTCTTTA GGATGGACTG TTCTGGTATC TGGTATGGT TTAGAGACTG TTAATAAGGG	1620
	ACATCACAAG GTGATGGGAT TCATTGGAAG CACTCTATTT CTGTTTTAAT GGTTTTATCC	1680
55	AATTTTGCCT TCCCAAGATT TTTGTTCTAC ATAAAAAGTT CATGCCACTT TTTAATATAA	1740
	AAAAATTTAA CAAAATTAAT GTATTTTCT CATTTTTTTC AACTTTTTTC TAAAGACTCT	1800
60	TTCTGTCAA CTCATGAAAA ATTTCTTCT ATGGCTTTTA TTCTAGATTG TCTTATTTTC	1860

482

10 TGTAAAAACC AATGACCACA TGACCACAAT CTTCACTAAC TCATACTGCA GTGAAAGTGT 1920  
 TAACCCTTAG GTAGTTTCTC TACAACTCTT TGCTATGGTG ATTTTAAAAA AAGTTTCCTA 1980  
 5 GGGAAAGTATC TCTGAGGGAA CAGGCAATCT GAAGGAACTG ACTATATTCT CCATGGCTAA 2040  
 GTCCATTAGG CCAAAAGNCT GGGTGGGTAT TGGTGTTCAN GCTGTCTATT GGCATATTAA 2100  
 10 AAACGTAGGC CGGANGGAAT AATTAGGTTG TNAAGCCGGC GGG 2143

## (2) INFORMATION FOR SEQ ID NO: 229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

25 CCTGGCCAC ATTGCTTCAT TGGCCTGGCC ATGCGCCTGT ACTATGGCAG CCGCTAGTCC 60  
 CTGACAACTT CCACCCTGAT TCCGGACCCT GTAGATTGGG CGCCACCACC AGATCCCCCT 120  
 CCCAGGCCTT CTTCCCTCTC CCATCAGCAG CCCTGTAACA AGTGCCCTGT GAGAAAAGCT 180  
 30 GGAGAAGTGA GGGCAGCCAG GTTATTCTCT GGAGGTTGGT GGATGAAGGG GTACCCTAGG 240  
 AGATGTGAAG TGTGGGTTTG GTTAAGGAAA TGCTTACCAT CCCCCACCCC CAACCAAGTT 300  
 35 CTTCCAGACT AAAGAATTAA GGTAACATCA ATACCTAGGC CTGAGAAATA ACCCCATCCT 360  
 TGTGGGCAG CTCCTTGCTT TGTCTGCTAT GAACAGAGTT GATGAAAGTG GGGTGTGGGC 420  
 AACAGTGGC TTTCTTGCC TACTTTAGTC ACCCAGCAGA GGCCTGGAG CTGGCTAGTC 480  
 40 CAGCCCAGCC ATGGTGCATG ACTCTTCCAT AAGGGATCCT CACCCTTCCA CTTCATGCA 540  
 AGAAGGCCCC GTTGCCACAG ATTATACAAC CATTACCCA ACCACTCTGA CAGTCTCCTC 600  
 45 CAGTTCAGC AATGCCTAGA GACATGCTCC CTGCCCTCTC CACAGTGTG CTCCCCACAC 660  
 CTAGCCTTTG TTCTGGAAAC CCCAGAGAGG GCTGGGCTTG ACTCATCTCA GGGAAATGTAG 720  
 CCCCTGGGCC CTGGCTTAAG CCGACACTCC TGACCTCTCT GTTCACCCCTG AGGGCTGTCT 780  
 50 TGAAGCCCCG TACCCACTCT GAGGCTCCTA GGAGGTACCA TGCTTCCCTAC TCTGGGGCCT 840  
 GCCCCTGCCT AGCAGTCTCC CAGCTCCCAA CAGCCTGGGG AAGCTCTGCA CAGAGTGACC 900  
 55 TGAGACCAGG TACAGGAAAC CTGTAGCTCA ATCAGTGTCT CTTTAACTGC ATAAGCAATA 960  
 AGATCTTAAT AAAGTCTTCT AGGCTGTAGG GTGGTTCTTA CAACCACAGC CAAAAAATA 1020  
 AAAAA 1025

60



## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

GGCCACGGCT CCGCCACGC GTCCGGCGGT GCGGAGTATG GGGCGCTGAT GGCATGGAG 60  
GGCTACTGGC GCTTCCTGGC GCYGCTGGG TCGGCACTGC TCGTCGGCTT CCTGTGGTG 120  
ATSTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGGAGCGCA 180  
CTAGAGTTTA ACTGGCACCC AGTGCTSATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC 240  
GCATCATCGT CTACAGACTG CCGTGGACCT GGAAATGCAG CAAGCTCCTG ATGAAATCCA 300  
TCCATGCAGG GTTAAATGCA GTTGCTGCCA TTCTTGCAAT TATCTCTGTG GTGGCCGTGT 360  
TTGAGAACCA CAATGTTAAC AATATAGCCA ATATGTACAG TCTGCACAGC TGGGTGGAC 420  
TGATAGCTGT CATATGCTAT TTGTTACAGC TTCTTTCAGG TTTTTCAGTC TTTCTGCTTC 480  
CATGGGCTCC GCTTCTCTC CGAGCATTTC TCATGCCCAT ACATGTTTAT TCTGGAATTG 540  
TCATCTTTGG AACAGTGATT GCAACAGCAC TTATGGGATT GACAGAGAAA CTGATTTTTT 600  
CCCTGAGAGA TCCTGCATAC AGTACATTCC CGCCAGAAGG TGTTTTCGTA AATACGCTTG 660  
GCCTTCTGAT CCTGGTGTTC GGGGCCCTCA TTTTGTGGAT AGTCACCAGA CCGCAATGGA 720  
AACGTCCTAA GGAGCCAAAT TCTACCATTC TTCATCCAAA TGGAGGCACT GAACAGGGAG 780  
CAAGAGGTTT CATGCCAGCC TACTCTGGCA ACAACATGGA CAAATCAGAT TCAGAGTTAA 840  
ACATGAAGT AGCAGCAAGG AAAAGAACT TAGCTCTGGA TGAGGCTGGG CAGAGATCTA 900  
CCATGTAAAA TGTGTAGAG ATAGAGCCAT ATAACGTCAC GTTTCAAAAC TAGCTCTACA 960  
GTTTTGCTTC TCCTATTAGC CATATGATAA TTGGGCTATG TAGTATCAAT ATTACTTTA 1020  
ATCACAAAGG ATGGTTTCTT GAAATAATTT GTATTGATTG AGGCCTATGA ACTGACCTGA 1080  
ATTGGAAAGG ATGTGATTAA TATAAATAAT AGCAGATATA AATTGTGGTT ATGTTACCTT 1140  
TATCTTGTG AGGACCACAA CATTAGCAGC GTGCCTTGTG CAAATAGAT ACTCAATATG 1200  
TGAATATGTG TCTACTAGTA GTTAATTGGA TAACTGGCA GCATCCCTGA 1250

## (2) INFORMATION FOR SEQ ID NO: 231:

## (i) SEQUENCE CHARACTERISTICS:

484

(A) LENGTH: 1811 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

	CNGNCAGTAC CGGTCNGATT CCCGGGTGCA CCCACGCGTC CGCTGCATTG CAGGGCCTTT	60
10	CAGTGGCTTT CATCTGGAAG TTCCTGGATA ACATGTTCCA TGTCTTGATG GCCCAGGTTA	120
	CCASTGTGCAT TATCACAACA GTGTCTGTCC TGGTCTTTGA CTTCAAGGCC TCCCTGGAAT	180
15	TTTTCTTGA AGCCSCATCA GTCSTYCTCT CTATATTTAT TTATAATGCC AGCAAGCCTC	240
	AAGTTCGCGA ATACGCACCT AGGCAAGAAA GGATCCGAGA TCTAAGTGGC AATCTTTGGG	300
	AGCGTTCCAG TGGGGATGGA GAAGAACTAG AAAGACTTAC CAAACCCAG AGTGATGAGT	360
20	CAGATGAAGA TACTTTCTAA CTGGTACCCA CATAGTTTGC AGCTCTCTTG AACCTTATTT	420
	TCACATTTTC AGTGTTTGTA ATATTTATCT TTTCACTTTG ATAAACCGA AATGTTCTA	480
25	AATCCTAATA TTCTTTGCAT ATATCTAGCT ACTCCCTAAA TGGTTCCATC CAAGGCTTAG	540
	AGTACCCAAA GGCTAAGAAA TTCTAAAGAA CTGATACAGG AGTAACAATA TGAAGAATTC	600
	ATTAATATCT CAGTACTTGA TAAATCAGAA AGTTATATGT GCAGATTATT TTCCTTGGCC	660
30	TTCAAGCTTC CAAAAACTT GTAATAATCA TGTTAGCTAT AGCTTGTATA TACACATAGA	720
	GATCAATTTG CCAAATATTC ACAATCATGT AGTTCTAGTT TACATGCCAA AGTCTTCCT	780
35	TTTAAACATT ATAAAAGCTA GGTGTCTCT TGAATTTGA GGCCCTAGAG ATAGTCATTT	840
	TGCAAGTAAA GAGCAACGGG ACCCTTTCTA AAAACGTTGG TTGAAGGACC TAAATACCTG	900
	GCCATACCAT AGATTTGGGA TGATGTAGTC TGTGCTAAAT ATTTTGCTGA AGAAGCAGTT	960
40	TCTCAGACAC AACATCTCAG AATTTTAATT TTTAGAAAT CATGGGAAAT TGGATTTTGT	1020
	TAATAATCTT TTGATGTTTT AAACATGGT TCCCTAGTCA CCATAGTTAC CACTTGTATT	1080
45	TTAAGTCATT TAAACAAGCC ACGGTGGGGC TTTTCTCTCC TCAGTTTGAG GAGAAAAATC	1140
	TTGATGTCAT TACTCCTGAA TTATTACATT TTGGAGAATA AGAGGGCATT TTATTTTATT	1200
	AGTTACTAAT TCAAGCTGTG ACTATGTAT ATCTTTCCAA GAGTTGAAAT GCTGGCTTCA	1260
50	GAATCATACC AGATTGTCAG TGAAGCTGAT GCCTAGGAAC TTTTAAAGG ATCCTTTCAA	1320
	AAGGATCACT TAGCAACAC ATGTTGACTT TTAAGTGAT TATGAATATT AATACTCTAA	1380
55	AAATAGAAAG ACCAGTAATA TATAAGTCAC TTTACAGTGC TACTTCACAC TTAAAAGTGC	1440
	ATGGTATTTT TCATGGTATT TTGCATGCAG CCAGTTAACT CTCGTAGATA GAGAAGTCAG	1500
	GTGATAGATG ATATTAAAAA TTAGCAAACA AAAGTGACTT GCTCAGGGTC ATGCAGCTGG	1560
60	GTGATGATAG AAGAGTGGGC TTAACTGGC AGGCCTGTAT GTTTACAGAC TACCATACTG	1620

485

TAAATATGAG CTTTATGGTG TCATTCTCAG AAACCTTATAC ATTTCTGCTC TCCTTTCTCC 1680  
TAAGTTTCAT GCAGATGAAT ATAAGGTAAT ATACTATTAT ATAATTCATT TGTGATATCC 1740  
ACAATAATAT GACTGGCAAG AATTGGTGA AATTGTGAAT TAAATAATT ATTAAACCTA 1800  
AAAAAAAAAN N 1811

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CTGACCTCAT GCGGTAGAGC CTAGCAACAG CGCAGGCTCC CAGCCGAGTC CGTTATGGCC 60  
GCTGCCGTCC CGAAGAGGAT GAGGGGGCCA GCACAAGCGA AACTGCTGCC CGGGTCGGCC 120  
ATCCAAGCCC TTGTGGGGTT GCGCGGSCCG CTGGTCTTGG CGCTCCTGCT TGTGTCCGCC 180  
GCTCTATCCA GTGTTGTATC ACGGACTGAT TCACCGAGCC CAACCGTACT CAACTCACAT 240  
ATTTCTACCC CAAATGTGAA TGCTTTAACA CATGAAAACC AAACCAAACC TTCTATTTCC 300  
CAAATCAGCA CCACCCTCCC TCCCACGACG AGTACCAAGA AAAGTGGAGG AGCATCTGTG 360  
GTCCCTCATC CCTCGCTTAC TCCTCTGTCT CAAGAGGAAG CTGATAACAA TGAAGATCCT 420  
AGTATAGAGG AGGACGATCT TCTGATGCTG AACAGTTCTC CATCCACAGC CAAAGACACT 480  
CTAGACAATG GCGATTATGG AGAACCAGAC TATGACTGGA CCACGGGCCC CAGGGACGAC 540  
GACCAGTCTG ATNGACACCT TGAAGAAAAA CAGGGGTTAC ATGGAATTTG AACAGTCAGT 600  
GAAATCTTTT AAGATGCCAT CCTCAAATAT AGAAGAGGAA GACAGCCATT TCTTTTTCa 660  
TCTTATTATT TTTGCTTTTT GCATTGCTGT TGTTTACATT ACATATCACA ACAAAGGAA 720  
GATTTTTCTT CTGTTTCAA GCAGGAAATG GCGTGATGGC CTTTGTTCa AAACAGTGA 780  
ATACCATCGC CTAGATCAGA ATGTTAATGA GGCAATGCCT TCTTTGAAGA TTACCAATGA 840  
TTATATTTTT TAAAGCACTG TGATTTGAAT TTGCTTATGT AATTTTATTT GCTTGACTTT 900  
TTATATGATA TTGTGCAAT GTTTGCCATA GGCAATTGGT ACTTAAATGA GAGGTGAGTC 960  
TCTGTTTTGC CTGGGTGCTT TGGAAATTAA ATGTCACAAA CGAGTATATA ATTTTTATC 1020  
TGTACTTTTA GAGCTGAGTT TAATCAGGTG TCCAAAATGT GAGTTAAACA TTACCTTATA 1080  
TTTACACTGT TAGTTTTTAT TGTTTTAGAT TTATTATGCT TCTTCTGGAA GTATTAGTGA 1140

486

TGCTACTTTT AAAAGATCCC AAACCTGTAA CTAAATCTCG ACATATCTGT TACTGCTGAC 1200  
 TCACATTGAT TCTCCGCCAT TCAAATACTA TTTTATATCC ACATTTTTTT TTGTTCCCAA 1260  
 5 ACTGTAATGT ACAAGCATAT GTGTGATAAT GCTTTGGATT TGAGTAATAT TTTTTTTTCT 1320  
 TCCAAGAAAA CTGCTTTGGA TATTTTTAGA TAATTTAAAC ATAATTTAGG ATAATGATAT 1380  
 10 TGCTCAATCT GACCACAATT TTAGGTAAAA CATTAAATGT GTCAAGAAAT CTGGCAACA 1440  
 GAGACTCTGC AGCTTCAGT GGACATAGAT AAAATGTTAC AGAGATACTA TTTTTTTGGT 1500  
 TGAATTACT ATATTAAAT TAGAAGCAGA AACTGGTAAA ATGTTAAATA CATGTACAAT 1560  
 15 TGCTTTTAGT TAGCAATTGA TTGTAGCATG GGTTCCTCCA AGGTTTCAAG CAATGGGCAG 1620  
 AGTTTAAAT TATATCAGAT TCGTTACTT CGTTTATTAT TTTACAGTAA ATTGAATAA 1680  
 20 ATCTTAGGGG TCATTATCAC TTAAATAATA CTGTACCTAG GTCTTTCAA TTAAATTAT 1740  
 ACCTGAATGA AGTTGTTTGT ATACATAAAG GATATTTGTG TACAATTACC TTTTTTCCCC 1800  
 CACACTTGT TTCTTTGTT TTGTTTTTA TGGCAACTGG AAAGTATTTA CTATGGGATT 1860  
 25 CATTTATGTC TGTCTTCTA TCATAAAGAA TTGATCAATA TGTAAATATG TGATTTGAAC 1920  
 CATGGTTGAC TTACAAGTGT CACTACAGCT TTTTAGAAAA CATAGCCCTA ATATATGTTA 1980  
 AGCAGGACCC GGGTGAGCCA GTGGGCTGCG GCTTTATGTA GAGCTGGAAG AAGGCCGTCC 2040  
 30 ATCCTGTCTC TTGGCGGAC AGTGTACTTT CCTAATAGG AAGGGAAGCA CAATCGAAAT 2100  
 ACCCTGAAC CGTTTATTG CAGTAATTT TTTATATCT GAACTATTA TTAAATATT 2160  
 35 TGAATAAGAT TTTAAAAAT AAATGGCAA GATATAATC TAAAAAANA AAAAAAANA 2220  
 AAAAAAANA AAAAAAANA AAAAAAANA AAAAAAANA AAAAAAANA N 2271

40

(2) INFORMATION FOR SEQ ID NO: 233:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

55

60

CTTCGGGTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC 60  
 TCTCCCTGGC GTTTGGTAC CTCTGCTTCA TTCTCCACCG CGCTATGGT CCCTCTTGA 120  
 GCCAGCGTGG CCGGCTGGC GGCTCCCGG TGGTGAGAGA GCGGTCCGG AACGATGAAG 180  
 GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGCTT CCGTCTCTCT CCTGCTGTTG 240  
 CTGCCTGAAC TAAGCGGTC CCTGGMAGTC CTGCTGCAGC CAGCTGAGGC CCGGCCAGGT 300

487

YTTGGGCTCT CTGACCCCTAG ACCAGGACAT TACCGCCGCT GCCACCGGGC CCTWACCCCT 360  
 GCCCAGCAGC CGGGCCGTGG TGTGGCTGAA GCTGCGGGGG CGCGCGGGCT CCGAGGGAGG 420  
 5 CAATGGCAGC AACCCCTGTGG CCGGGCTTGA GACGGACGAT CACGGAGGGA AGCCCGGGGA 480  
 ARGCTCGGTG GGTGGCGGGC TTGCTGTGAG CCCCAACCCCT GCGGACAAGC CCATGACCCA 540  
 10 GCGGGCCCTG ACCGTGTGTA TGGTGGTGAG CGCGCGGGTG CTGGTGTACT TCGTGGTCAG 600  
 GACCGTCAGG ATGAGAAGAA GAAACCGAAA GACTAGGAGA TATGGAGTTT TGGACACTPA 660  
 CATAGAAAAT ATGGAATTGA CACCTTTAGA ACAGGATGAT GAGGATGATG ACAACACGTT 720  
 15 GTTTGATGCC AATCATCCTC GAAGATAAGA ATGTGCCTTT TGATGAAAGA ACTTTATCTT 780  
 TGTACAATGA AGAGTGGAAAT TTCTATGTTT AAGGAATAAG AAGCCACTAT ATCAATGTTG 840  
 20 GGGGGGTATT TAAGTTACAT ATATTTNAAC AACCTTTAAT TTGCTGTTGC AATAAATACC 900  
 GTATCCTTTT ATTATATCTT TATATGTATA GAAGTACTCT GTTAATGGGC TCAGAGATGT 960  
 TGGGGATAAA GTTACTGTGA ATAATTTATC TGTTTGAAAA TTAATAATAA ACGGTGTTTT 1020  
 25 CTGRTCGGTT TTTGTTTCCT GCTTACCATA TGATTGTAAA TTGTTTTATG TATTAATCAG 1080  
 TTAATGCTAA TTATTTTTGC TGATGTCATA TGTAAAGAG CTATAAATTC CAACAACCAA 1140  
 30 CTGGTGTGTA AAAATAATTT AAAATYTCCT TTAAGTAAAG GTATTTCCCA TTTTGTGGG 1200  
 GAAAAGAAGC CAAATTTATT ACTTTGTGTT GGGGTTTTTA AAATATTAAG AAATGTCTAA 1260  
 GTTATTGTTT GCAAAACAAT AAATATGATT TAAATCTC TTAACAAAAA AAAAAAANC 1320  
 35 CCGGGGGGGG GCGCCGGN 1338

40

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

45

Met Leu Ser Thr Gly Ile Glu Val Ala Arg Pro Pro Ala Thr Leu Leu  
 1 5 10 15

50

Gly Leu Met Phe Val Leu Thr Gly Met Pro Arg Gly Leu Arg Xaa  
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

60

488

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

5 Met Asn Val Val Ile Val Ile Ile Leu Phe Ser Phe Asp Ser Val Gly  
 1 5 10 15  
 Thr Met Phe Ser Cys Asn Arg Ile Pro Lys Ile Thr Val Leu Asn Lys  
 20 25 30  
 10 Leu Lys Phe Xaa Cys Glu Val Leu Leu Arg Ile Gln Thr Ile Gln Gly  
 35 40 45  
 Phe Tyr Arg Cys Thr Arg Ile Ser Arg Tyr Lys Gly Ile Phe Pro Asp  
 50 55 60  
 15 Phe Cys Gln Ser Gln Cys Met Gly Cys Asn Pro Glu Ser Xaa Met Ala  
 65 70 75 80  
 20 Val Pro Ala Leu Val Thr Pro Ile Leu Ala His Arg Lys Lys Glu Lys  
 85 90 95  
 Gly Met Cys Leu Phe Thr Leu Ile Ile Ala Pro Thr Arg Cys Thr His  
 100 105 110  
 25 Tyr Phe Cys Xaa  
 115

30

(2) INFORMATION FOR SEQ ID NO: 236:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

40 Met Ser Ser Ala Lys Ile Val Arg Gln Arg Gly Ala Val Pro Thr Tyr  
 1 5 10 15  
 Tyr Thr Thr Glu Ala Gly Glu Ile Ile Phe Leu Val Leu Asn Trp Ser  
 20 25 30  
 45 Leu Ser Ile Leu His Ile Val Asp Val Leu Cys Ser Lys Pro Glu Lys  
 35 40 45  
 Ser Val Thr Glu Asp Ala Ala Ser Gly Leu Ser Gln Arg Met Thr Ala  
 50 55 60  
 50 Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys Pro Ile Leu  
 65 70 75 80  
 Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His Ser Phe Ile  
 85 90 95  
 55 His Ser Ser Asn Ile Cys Xaa  
 100

60

439

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

5 Met Ile Leu Phe Pro Gln Xaa Ala Leu Arg Leu Gly Xaa Trp Pro Arg  
 1 5 10 15  
 Thr Trp Ser Ile Leu Xaa Lys Tyr Ser Val Asn Phe Phe Ser Ala Tyr  
 20 25 30  
 15 Ser Pro Met Gly Ala Val Gly Thr Glu Phe  
 35 40

20

## (2) INFORMATION FOR SEQ ID NO: 238:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

25 Met Ile Ile Leu Leu Leu Phe Met Leu Leu Asn Asn Val Val Leu Val  
 30 1 5 10 15  
 Gln Glu Asp Asn Cys Gln Arg Lys Asn Thr Val Gln Glu Arg Arg Xaa  
 20 25 30  
 35 Trp Ser Gln Trp Xaa  
 35

40

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

45 Met Ala Ala Xaa Pro Pro Gly Cys Thr Pro Pro Xaa Leu Leu Asp Ile  
 50 1 5 10 15  
 Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly Gln Pro Val Pro Val Glu  
 20 25 30  
 55 Cys Arg His Arg Leu Glu Val Ala Gly Pro Arg Lys Gly Pro Leu Ser  
 35 40 45  
 Pro Ala Trp Met Pro Ala Tyr Ala Cys Gln Arg Pro Thr Pro Leu Thr  
 50 55 60  
 60 His His Asn Thr Gly Leu Ser Glu Leu Leu Glu His Gly Val Cys Glu

490

65					70						75					80
Glu	Val	Glu	Arg	Val	Arg	Arg	Ser	Glu	Arg	Tyr	Gln	Thr	Met	Lys	Val	
				85					90					95		
Arg	Arg	Ala	Gly	Leu	Gly	Pro	Thr	Pro	Gly	Met	Ser	Cys	Pro	Gly	Asn	
			100					105						110		
Asp	Asn	Thr	Val	His	Thr	Met	His	Gly	Glu	Ala	Asn	Arg	Gly	Ser	Kaa	
			115				120					125				

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(E) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

25 Met Ser Ile Leu Cys Cys Pro Xaa Leu Phe Phe Ser Phe Cys
    1                      5              10              15

Ile Ser Ser Gly Ser Cys Pro Phe Ser His Val Ser Gln Leu Ser Phe
    20                      25                      30

30 Ile Ala Thr Phe Ser Gln Ser Ser Pro Val Leu Leu Val Pro Ala Tyr
    35                      40                      45

Asn Thr Tyr Leu Ser Phe Leu Ala Phe Leu Asp Cys Ala Ser Leu Thr
    50                      55                      60

35 Ser Thr Xaa
    65

```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```

50 Met Ser Thr Phe Gln Leu Leu Leu Ile Leu Ala Gln Ser Thr Tyr
    1          5          10          15

Lys Ile Lys Ser Lys Pro Leu His Met Thr Asn His Thr Leu Leu Asn
    20          25          30

55 Ser Pro Gly Leu Asn Pro Ser Ser Pro Thr Leu Asn Phe Lys Thr Gln
    35          40          45

Gln His Glu Ser Val Ser Tyr Ala Cys Cys His Met Arg Ser Leu His
60  30          55          60

```



491.

His Ala Phe Ala Xaa  
65

5

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

15 Met Val Ser Val Val Leu Ile Phe Ser Phe Leu Ser Leu Thr Ile Ser  
 1 5 10 15  
 Thr Thr Ala Ser Ala Tyr Asn Gly Asn Asp Thr Gln Gly Trp Asn Asp  
 20 25 30  
 20 Lys Phe His Xaa Xaa Ser Val Lys Thr Gln Thr Xaa  
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

35 Met Ile Ser Asp Ala Gly Ala Gly Phe Gly Val Phe Leu Leu Val Pro  
 1 5 10 15  
 Arg Ala Gly His Cys Trp Gly Ala Gly Lys Pro Leu Pro Ser Cys Pro  
 20 25 30  
 40 Ser Val Ala Ser Ile Pro Ser Trp Val Leu Pro Ser Phe Leu Glu Arg  
 35 40 45  
 Gly Arg Xaa  
 50

45

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

55

Met Val Gln Thr Ile Gln Asp Phe Leu Ser Leu Phe Ser Thr Pro Ile  
 1 5 10 15  
 Phe Leu Leu Leu Leu Met Phe Glu Thr Leu Ser Leu Ala Pro Ala Trp  
 20 25 30  
 60

Leu Lys Pro Leu Arg Val Thr Ser His Ser Xaa  
35 40

5

## (2) INFORMATION FOR SEQ ID NO: 245:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

15

Met Ile Leu Met Pro Gly Leu Gly Thr Ser Arg Gln Arg Ser Val Pro  
1 5 10 15

Phe Val Pro Thr Leu Asn Ala Ser Thr Pro Gly Ala Met Thr Gly Pro  
20 25 30

20

Thr Ala Thr Leu Thr Ser Cys Gln Trp Thr Thr Ala Cys Arg Val Ser  
35 40 45

25

Trp Ala Asn Gly Trp Thr Ser Leu Arg Thr Phe Arg Xaa  
50 55 60

30

## (2) INFORMATION FOR SEQ ID NO: 246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Met Ser His His Ala Gln Pro Arg Phe Leu Leu Ile Thr Met Leu Leu  
1 5 10 15

40

Gln Glu Ala Lys Pro Val Ser Asn Ile Pro His Leu Leu Glu Ser Trp  
20 25 30

Tyr Phe Gly Xaa  
35

45

## (2) INFORMATION FOR SEQ ID NO: 247:

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Met Asn Ser Leu Phe Trp Met Ile Leu Leu Pro Val Ser Gln Asp Gln  
1 5 10 15

60

Val Val Glu Gly Leu Gln Gly Gly Phe Ser Gln Ile His Met Arg Ile  
20 25 30

493

Leu Arg Lys His Leu Xaa  
35

5

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

15 Met Ser Arg Ser Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala  
1 5 10 15  
Ala Ser Ile Tyr Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala  
20 20 25 30  
Leu His Gln Gly Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile  
35 40 45  
Leu Leu Lys Leu Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg  
25 50 55 60  
Met Gln Asp Leu Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala  
65 70 75 80  
30 Trp Val Ser Leu Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr  
85 90 95  
Ile Phe Gln Glu Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu  
100 105 110  
35 Asn Gly Gln Ala Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala  
115 120 125  
Glu Gly Leu Leu Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu  
40 130 135 140  
Thr Leu Val Asn Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro  
145 150 155 160  
45 Glu Val Thr Asn Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser  
165 170 175  
His Pro Phe Ile Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg  
180 185 190  
50 Leu Val Leu Gln Tyr Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser  
195 200 205  
55 Gly Pro Xaa  
210

60

(2) INFORMATION FOR SEQ ID NO: 249:

494

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Met Glu Asp Ser Glu Ala Leu Gly Phe Glu His Met Gly Leu Asp Pro  
 1 5 10 15

Arg Leu Leu Gln Ala Val Thr Asp Leu Gly Trp Ser Arg Pro Thr Leu  
 20 25 30

Ile Gln Glu Lys Ala Ile Pro Leu Ala Leu Glu Gly Lys Asp Leu Leu  
 35 40 45

Ala Arg Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Tyr Ala Ile Pro  
 50 55 60

Met Leu Gln Leu Leu Leu His Arg Lys Ala Thr Gly Pro Val Val Glu  
 65 70 75 80

Gln Ala Val Arg Gly Leu Val Leu Val Pro Thr Lys Glu Leu Ala Arg  
 85 90 95

Gln Ala Gln Ser Met Ile Gln Gln Leu Ala Thr Tyr Cys Ala Arg Asp  
 100 105 110

Val Arg Val Ala Asn Val Ser Ala Ala Glu Asp Ser Val Ser Gln Arg  
 115 120 125

Ala Val Leu Met Glu Lys Pro Asp Val Val Val Gly Thr Pro Ser Arg  
 130 135 140

Ile Leu Ser His Leu Gln Gln Asp Ser Leu Lys Leu Arg Asp Ser Leu  
 145 150 155 160

Glu Leu Leu Val Val Asp Glu Ala Asp Leu Leu Phe Ser Phe Gly Phe  
 165 170 175

Glu Glu Glu Leu Lys Ser Leu Leu Cys His Leu Pro Arg Ile Tyr Gln  
 180 185 190

Ala Phe Leu Met Ser Ala Thr Phe Asn Glu Asp Val Gln Ala Leu Lys  
 195 200 205

Glu Leu Ile Leu His Asn Pro Val Thr Leu Lys Leu Gln Glu Ser Gln  
 210 215 220

Leu Pro Gly Pro Asp Gln Leu Gln Gln Phe Gln Val Val Cys Glu Thr  
 225 230 235 240

Glu Glu Asp Lys Phe Leu Leu Leu Tyr Ala Leu Leu Lys Leu Ser Leu  
 245 250 255

Ile Arg Gly Lys Ser Leu Leu Phe Val Asn Thr Leu Glu Arg Ser Tyr  
 260 265 270

Arg Leu Arg Leu Phe Leu Glu Gln Phe Ser Ile Pro Thr Cys Val Leu  
 275 280 285

60

495

Asn Gly Glu Leu Pro Leu Arg Ser Arg Cys His Ile Ile Ser Gln Phe  
 290 295 300  
 5 Asn Gln Gly Phe Tyr Asp Cys Val Ile Ala Thr Asp Ala Glu Val Leu  
 305 310 315 320  
 Gly Ala Pro Val Lys Gly Lys Arg Arg Gly Arg Gly Pro Lys Gly Asp  
 325 330 335  
 10 Lys Ala Ser Asp Pro Glu Ala Gly Val Ala Arg Gly Ile Asp Phe His  
 340 345 350  
 His Val Ser Ala Val Leu Asn Phe Asp Leu Pro Pro Thr Pro Glu Ala  
 355 360 365  
 15 Tyr Ile His Arg Ala Gly Arg Thr Ala Arg Ala Asn Asn Pro Gly Ile  
 370 375 380  
 20 Val Leu Thr Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile  
 385 390 395 400  
 Glu Glu Leu Leu Ser Gly Glu Asn Arg Gly Pro Ile Leu Leu Pro Tyr  
 405 410 415  
 25 Gln Phe Arg Met Glu Glu Ile Glu Gly Phe Arg Tyr Arg Cys Arg Asp  
 420 425 430  
 Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu Lys  
 435 440 445  
 30 Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr Phe  
 450 455 460  
 Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro Leu  
 465 470 475 480  
 His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr Leu  
 485 490 495  
 40 Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg Lys  
 500 505 510  
 Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln Asn  
 515 520 525  
 45 Pro Leu Arg Ser Phe Lys His Lys Gly Lys Lys Phe Arg Pro Thr Ala  
 530 535 540  
 50 Lys Pro Ser Xaa  
 545

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Met Thr Thr Val Pro Pro Ser Pro Arg Pro Met Ser Arg Pro Ser Glu  
 1 5 10 15  
 5 Arg Asn Met Arg Arg Pro Arg Gly Pro Ser Pro Leu Pro Ala Ser Pro  
 20 25 30  
 Arg Asn Ser Thr Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe  
 35 40 45  
 10 Leu Asn Val Phe Met Ser Gly Arg Ser Arg Ser Ser Ala Glu Ser  
 50 55 60  
 Phe Gly Leu Phe Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr  
 15 65 70 75 80  
 His Arg Ala Ile Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu  
 85 90 95  
 20 Leu Glu Val Asp Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr  
 100 105 110  
 Trp Tyr Glu Ala Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro  
 115 120 125  
 25 Ala Tyr Tyr Ala Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala  
 130 135 140  
 Leu Ala Lys Asn Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu  
 30 145 150 155 160  
 Gly Ser Val Gln Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala  
 165 170 175  
 35 Ala Met Gln Lys Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn  
 180 185 190  
 Pro Pro Ser Ser Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile  
 195 200 205  
 40 Gly Val Lys Ala Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser  
 210 215 220  
 His Phe Phe Gln Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys  
 45 225 230 235 240  
 Asn Asn Lys Tyr Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg  
 245 250 255  
 50 Phe Ala Cys His Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala  
 260 265 270  
 Glu Ser Val Gly Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu  
 275 280 285  
 55 Tyr Thr Cys Pro Thr Glu Asp Ile Tyr Leu Glu  
 290 295  
 60

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Leu Leu Tyr Leu Leu Lys Val Xaa Val Ile Phe Val Phe Ser Ser Ser  
 1 5 10 15  
 Lys Gly Val Thr Leu Val Ser Met Asn Leu Thr Ser Phe Phe Val Ser  
 20 25 30  
 Ser Val Leu Ala Cys Phe Ser Xaa  
 35 40

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Met Pro Ala Ser Ser Leu Glu Ser Arg Ser Phe Leu Leu Ala Lys Lys  
 1 5 10 15  
 Ser Gly Glu Asn Val Ala Lys Phe Ile Ile Asn Ser Tyr Pro Lys Tyr  
 20 25 30  
 Phe Gln Lys Asp Ile Ala Glu Pro His Ile Pro Cys Leu Met Pro Glu  
 35 40 45  
 Tyr Phe Glu Pro Gln Ile Lys Asp Ile Ser Glu Ala Ala Leu Lys Glu  
 50 55 60  
 Arg Ile Glu Leu Arg Lys Val Lys Ala Ser Val Asp Met Phe Asp Gln  
 65 70 75 80  
 Leu Leu Gln Ala Gly Thr Thr Val Ser Leu Glu Thr Thr Asn Ser Leu  
 85 90 95  
 Leu Asp Xaa Leu Cys Tyr Tyr Gly Asp Gln Glu Pro Ser Thr Asp Tyr  
 100 105 110  
 His Phe Gln Gln Thr Gly Gln Ser Glu Ala Leu Glu Glu Glu Asn Asp  
 115 120 125  
 Glu Thr Ser Arg Arg Lys Ala Gly His Gln Phe Gly Val Thr Trp Arg  
 130 135 140  
 Ala Lys Asn Asn Ala Glu Arg Ile Phe Ser Leu Met Pro Glu Lys Asn  
 145 150 155 160  
 Glu His Ser Tyr Cys Thr Met Ile Arg Gly Met Val Lys His Arg Ala  
 165 170 175

Tyr Glu Gln Ala Leu Asn Leu Tyr Thr Glu Leu Leu Asn Asn Arg Leu  
 180 185 190  
 5 His Ala Asp Val Tyr Thr Phe Asn Ala Leu Ile Glu Ala Thr Val Cys  
 195 200 205  
 Ala Ile Asn Glu Lys Phe Glu Glu Lys Trp Ser Lys Ile Leu Glu Leu  
 210 215 220  
 10 Leu Arg His Met Val Ala Gln Lys Val Lys Pro Asn Leu Gln Thr Phe  
 225 230 235 240  
 Asn Thr Ile Leu Lys Cys Leu Arg Arg Phe His Val Phe Ala Arg Ser  
 245 250 255  
 15 Pro Ala Leu Gln Val Leu Arg Glu Met Lys Ala Ile Gly Ile Glu Pro  
 260 265 270  
 20 Ser Leu Ala Thr Tyr His His Ile Ile Arg Leu Phe Asp Gln Pro Gly  
 275 280 285  
 Asp Pro Leu Lys Arg Ser Ser Phe Ile Ile Tyr Asp Ile Met Asn Glu  
 290 295 300  
 25 Leu Met Gly Lys Arg Phe Ser Pro Lys Asp Pro Asp Asp Asp Lys Phe  
 305 310 315 320  
 Phe Gln Ser Ala Met Ser Ile Cys Ser Ser Leu Arg Asp Leu Glu Leu  
 325 330 335  
 30 Ala Tyr Gln Val His Gly Leu Leu Lys Thr Gly Asp Asn Trp Lys Phe  
 340 345 350  
 35 Ile Gly Pro Asp Gln His Arg Asn Phe Tyr Tyr Ser Lys Phe Phe Asp  
 355 360 365  
 Leu Ile Cys Leu Met Glu Gln Ile Asp Val Thr Leu Lys Trp Tyr Glu  
 370 375 380  
 40 Asp Leu Ile Pro Ser Ala Tyr Phe Pro His Ser Gln Thr Met Ile His  
 385 390 395 400  
 Leu Leu Gln Ala Leu Asp Val Ala Asn Arg Leu Glu Val Ile Pro Lys  
 405 410 415  
 45 Ile Trp Lys Asp Ser Lys Glu Tyr Gly His Thr Phe Arg Ser Asp Leu  
 420 425 430  
 50 Arg Glu Glu Ile Leu Met Leu Met Ala Arg Asp Lys His Pro Pro Glu  
 435 440 445  
 Leu Gln Val Ala Phe Ala Asp Cys Ala Ala Asp Ile Lys Ser Ala Tyr  
 450 455 460  
 55 Glu Ser Gln Pro Ile Arg Gln Thr Ala Gln Asp Trp Pro Ala Thr Ser  
 465 470 475 480  
 Leu Asn Cys Ile Ala Ile Leu Phe Leu Arg Ala Gly Arg Thr Gln Glu  
 485 490 495  
 60



499

Ala Trp Lys Met Leu Gly Leu Phe Arg Lys His Asn Lys Ile Pro Arg  
500 505 510

Ser Glu Leu Leu Asn Glu Leu Met Asp Ser Ala Lys Val Ser Asn Ser  
515 520 525

Pro Ser Gln Ala Ile Glu Val Val Glu Leu Ala Ser Ala Phe Ser Leu  
530 535 540

Pro Ile Cys Glu Gly Leu Thr Gln Arg Val Met Ser Asp Phe Ala Ile  
545 550 555 560

Asn Gln Glu Gln Lys Glu Ala Leu Ser Asn Leu Thr Ala Leu Thr Ser  
565 570 575

Asp Ser Asp Thr Asp Ser Ser Ser Asp Ser Asp Ser Asp Thr Ser Glu  
580 585 590

Gly Lys

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Met Lys Leu Asn Leu Cys Ile Pro Asn Trp Ala Arg Cys Pro Leu Leu  
1 5 10 15

Leu Leu Phe Pro Gln Leu Leu Pro Phe Gln Gly Glu Asp Asp Asp Pro  
20 25 30

Leu Lys Ala Lys Ala Ala Asn Leu Val Glu Ala Val Pro Trp Gly Ile  
35 40 45

Lys Ala Pro Ser Phe Gln Val Thr Cys Leu Val Arg Val Gln Leu Gln  
50 55 60

Ser Cys Thr Pro Ser Arg Pro Ser Thr Leu Leu Ala Thr Ser Gln Ser  
65 70 75 80

Pro Gly Arg Ile Ser Cys Tyr Ser Pro Leu Ser His Leu Pro Pro Val  
85 90 95

Thr Thr Ser Ile Gln Pro Ser Pro Val Met Val Pro Phe Gln Tyr Gln  
100 105 110

Ala Phe Leu Leu Gln Val Lys Glu Pro Ala Ala Gln Thr Leu Leu Gly  
115 120 125

Gln Gln Xaa  
130

500

## (2) INFORMATION FOR SEQ ID NO: 254:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Met Arg Tyr His Ala Gln Leu Ile Phe Cys Ile Phe Cys Xaa Phe Val  
 1 5 10 15  
 Phe Val Xaa Lys Xaa  
 20

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Met Asn Asp Asn Ser Pro Asn His Ser Ser Ser Tyr Leu Pro Leu Pro  
 1 5 10 15  
 Leu Thr Ile Val Ile Leu Gln Thr Gly His Lys Gly Thr Leu Xaa  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr Leu Trp Gly Leu  
 1 5 10 15  
 Phe Thr Ala Gln Arg Gln Lys Lys Glu Ser Thr Glu Glu Val Lys  
 20 25 30  
 Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys  
 35 40 45  
 Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu Ala Lys Asp Gly  
 50 55 60  
 Ser Lys Phe Tyr Cys Ser Arg Thr Gln Asn Glu Gly His Pro Lys Trp  
 65 70 75 80  
 Phe Val Leu Gly Val Gly Gln Val Ile Lys Gly Leu Asp Ile Ala Met  
 85 90 95  
 Thr Asp Met Cys Pro Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser  
 100 105 110

501

Phe Ala Tyr Gly Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp  
 115 120 125  
 5 Ala Thr Leu Ile Phe Glu Ile Glu, Leu Tyr Ala Val Thr Lys Gly, Pro  
 130 135 140  
 Arg Ser Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln  
 145 150 155 160  
 10 Leu Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys  
 165 170 175  
 Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu Asp  
 180 185 190  
 15 Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser Pro Lys  
 195 200 205  
 20 Glu Tyr Asn Val Tyr Gln His Asp Glu Leu Xaa  
 210 215

25 (2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Met Trp Val Ile Arg Val Phe Gln Lys Thr Phe Leu Phe Phe Val Leu  
 1 5 10 15  
 35 Phe Trp Ser Val His Cys Ile Ser Asp Lys Phe Gly Cys Leu Trp His  
 20 25 30  
 40 Val Cys Met Lys Arg Glu Gly Asp Xaa Asn Cys Leu Ser Phe Ser Xaa  
 35 40 45  
 Leu Xaa  
 50

45

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Met Pro Ser Gln Thr Glu Xaa Phe Ala Ala Cys Gly Gly His Ser Leu  
 1 5 10 15  
 55 Leu Leu Val Xaa Leu Pro Leu Gly Leu Pro Phe Cys Pro Arg Ala Ala.  
 20 25 30  
 60

502

Leu Cys Asp Leu Pro Phe Ser Leu Pro Ser Phe Pro Gly Gln Ala Arg  
 35 40 45  
 Arg Gly Gly Ala Glu Lys Gln Gly Ala Glu Gly Arg Gly Leu Gln Val  
 5 50 55 60  
 Lys Pro Arg Gly Gln Arg Thr Phe Gln Val Ser Arg Thr Ala Pro Ala  
 65 70 75 80  
 Ala Pro Arg Ser Arg Gln Pro Arg Pro Pro Ala Ala Leu Pro Ala Leu  
 10 85 90 95  
 Gly Phe Gly Gly Arg Gly Val Ala Lys Gly Arg Phe Leu Cys Phe Trp  
 100 105 110  
 Cys Leu Tyr Met Leu Arg Ile Asp Gln Xaa  
 115 120

20

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln Ser Leu Leu Pro  
 30 1 5 10 15  
 Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro Gly Glu Glu Asp  
 20 25 30  
 Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met Ala Lys Gly Ala  
 35 35 40 45  
 Arg Pro Gly Ala Xaa Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr Thr  
 40 50 55 60  
 Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys Thr Ala Leu Leu  
 65 70 75 80  
 Gly Ala Asn Gly Ala Gln Pro Xaa  
 45 85

50

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Met Ile Gln Val Ser Val Pro Leu Leu Thr Ile Met Ile Phe Leu Leu  
 1 5 10 15  
 Tyr Leu Gln Ile Gly Pro Gly Lys Leu Xaa  
 60

503

20

25

## 5 (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Met Leu Leu Asp Pro Phe Ile Leu Leu Phe Cys Leu Phe Ser Thr Ala  
 1 5 10 15

15

Ala Gln Ser Cys Leu Glu Phe Ile Tyr Ile Gln Phe Xaa  
 20 25

20

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Met Lys Phe Leu Ser Ile Leu Leu Asp Asp Asn Asn Phe Xaa Leu Met  
 1 5 10 15

30

Leu Met Leu Ala Pro Phe Gly Cys Leu Ala Phe Glu Arg Ser Met Lys  
 20 25 30

35

Met Arg Asn Gly Ala Leu Gly Leu Glu Glu Val Xaa  
 35 40

40

## (2) INFORMATION FOR SEQ ID NO: 263:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
 1 5 10 15

50

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys  
 20 25 30

55

Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg  
 35 40 45

Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His  
 50 55 60

60

Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp

504

	65		70		75		80									
	Val	Leu	Gly	Tyr	Val	Thr	Pro	Trp	Asn	Ser	His	Gly	Tyr	Asp	Val	Thr
					85					90					95	
5	Lys	Val	Phe	Gly	Ser	Lys	Phe	Thr	Gln	Ile	Ser	Pro	Val	Trp	Leu	Gln
				100					105						110	
10	Leu	Lys	Arg	Arg	Gly	Arg	Glu	Met	Phe	Glu	Val	Thr	Gly	Leu	His	Asp
			115					120						125		
	Val	Asp	Gln	Gly	Trp	Met	Arg	Ala	Val	Arg	Lys	His	Ala	Lys	Gly	Leu
		130					135						140			
15	His	Ile	Val	Pro	Arg	Leu	Leu	Phe	Glu	Asp	Trp	Thr	Tyr	Asp	Asp	Phe
		145				150					155					160
	Arg	Asn	Val	Leu	Asp	Ser	Glu	Asp	Glu	Ile	Glu	Glu	Leu	Ser	Lys	Thr
					165					170					175	
20	Val	Val	Gln	Val	Ala	Lys	Asn	Gln	His	Phe	Asp	Gly	Phe	Val	Val	Glu
				180					185						190	
	Val	Trp	Asn	Gln	Leu	Leu	Ser	Gln	Lys	Arg	Val	Thr	Asp	Gln	Leu	Gly
25			195					200						205		
	Met	Phe	Thr	His	Lys	Glu	Phe	Glu	Gln	Leu	Ala	Pro	Val	Leu	Asp	Gly
		210					215						220			
30	Phe	Ser	Leu	Met	Thr	Tyr	Asp	Tyr	Ser	Thr	Ala	His	Gln	Pro	Gly	Pro
		225				230					235					240
	Asn	Ala	Pro	Leu	Ser	Trp	Val	Arg	Ala	Cys	Val	Gln	Val	Leu	Asp	Pro
				245					250						255	
35	Lys	Ser	Lys	Trp	Arg	Ser	Lys	Ile	Leu	Leu	Gly	Leu	Asn	Phe	Tyr	Gly
			260					265							270	
	Met	Asp	Tyr	Ala	Thr	Ser	Lys	Asp	Ala	Arg	Glu	Pro	Val	Val	Gly	Ala
40			275					280						285		
	Arg	Tyr	Ile	Gln	Thr	Leu	Lys	Asp	His	Arg	Pro	Arg	Met	Val	Trp	Asp
		290					295						300			
45	Ser	Gln	Xaa	Ser	Glu	His	Phe	Phe	Glu	Tyr	Lys	Lys	Ser	Arg	Ser	Gly
		305				310					315					320
	Arg	His	Val	Val	Phe	Tyr	Pro	Thr	Leu	Lys	Ser	Leu	Gln	Val	Arg	Leu
				325						330					335	
50	Glu	Leu	Ala	Arg	Glu	Leu	Gly	Val	Gly	Val	Ser	Ile	Trp	Glu	Leu	Gly
			340					345						350		
	Gln	Gly	Leu	Asp	Tyr	Phe	Tyr	Asp	Leu	Leu	Xaa					
55			355					360								

(2) INFORMATION FOR SEQ ID NO: 264:

60

505

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Leu Pro Thr Lys Ile Leu Val Lys Pro Asp Arg Thr Phe Glu Ile Lys  
 1 5 10 15

10 Ile Gly Gln Pro Thr Val Ser Tyr Phe Leu Lys Ala Ala Ala Gly Ile  
 20 25 30

Glu Lys Gly Ala Arg Gln Thr Gly Lys Glu Val Ala Gly Leu Val Thr  
 35 40 45

15 Leu Lys His Val Tyr Glu Ile Ala Arg Ile Lys Ala Gln Asp Glu Ala  
 50 55 60

20 Phe Ala Leu Gln Asp Val Pro Leu Ser Ser Val Val Arg Ser Ile Ile  
 65 70 75 80

Gly Ser Ala Arg Ser Leu Gly Ile Arg Val Val Lys Asp Leu Ser Ser  
 85 90 95

25 Glu Glu Leu Ala Ala Phe Gln Lys Glu Arg Ala Ile Phe Leu Ala Ala  
 100 105 110

Gln Lys Glu Ala Asp Leu Ala Ala Gln Glu Glu Ala Ala Lys Lys Xaa  
 115 120 125

30

35

(2) INFORMATION FOR SEQ ID NO: 265:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

45 Met Leu Leu Gln Ile His Pro Leu Leu Pro Ser Pro Thr Ile Pro His  
 1 5 10 15

Ile Leu Leu Leu Phe Leu Tyr Pro Thr Phe Ser Ile Leu Glu His Ser  
 20 25 30

50 Cys Ser Tyr Cys Ile Glu Tyr Leu Trp Val Cys Leu Leu Phe Cys Leu  
 35 40 45

Ser Leu Trp Phe Leu Xaa  
 50

55

(2) INFORMATION FOR SEQ ID NO: 266:

60 (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Met Cys Leu Trp Cys Cys Gly Asp Val Cys Ser Gly Leu Ser Ser Leu  
 1 5 10 15

Leu Ser Leu Cys Val Cys Cys Val Val Leu Ala Val Cys  
 20 25

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Glu Gly Leu Arg Leu Leu Leu Ser Leu Pro Ala Ala Leu Pro Arg Ser  
 1 5 10 15

Cys Cys His Pro Arg Trp Leu Pro Val Xaa  
 20 25

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Met Phe His Gly Ile Pro Ala Thr Pro Gly Ile Gly Ala Pro Gly Asn  
 1 5 10 15

Lys Pro Glu Leu Tyr Glu Glu Val Lys Leu Tyr Lys Asn Ala Arg Glu  
 20 25 30

Arg Glu Lys Tyr Asp Asn Met Ala Glu Leu Phe Ala Val Val Lys Thr  
 35 40 45

Met Gln Ala Leu Glu Lys Ala Tyr Ile Lys Asp Cys Val Ser Pro Ser  
 50 55 60

Glu Tyr Thr Ala Ala Cys Ser Arg Leu Leu Val Gln Tyr Lys Ala Ala  
 65 70 75 80

Phe Arg Gln Val Gln Gly Ser Glu Ile Ser Ser Ile Asp Glu Phe Cys  
 85 90 95

Arg Lys Phe Arg Leu Asp Cys Pro Leu Ala Met Glu Arg Ile Lys Glu  
 100 105 110

Asp Arg Pro Ile Thr Ile Lys Asp Asp Lys Gly Asn Leu Asn Arg Cys  
 115 120 125



Ile Ala Asp Val Val Ser Leu Phe Ile Thr Val Met Asp Lys Leu Arg  
 130 135 140

5 Leu Glu Ile Arg Ala Met Asp Glu Ile Gln Pro Asp Leu Arg Glu Leu  
 145 150 155 160

Met Glu Thr Met His Arg Met Ser His Leu Pro Pro Asp Phe Glu Gly  
 165 170 175

10 Arg Gln Thr Val Ser Gln Trp Leu Gln Thr Leu Ser Gly Met Ser Ala  
 180 185 190

15 Ser Asp Glu Leu Asp Asp Ser Gln Val Arg Gln Met Leu Phe Asp Leu  
 195 200 205

Glu Ser Ala Tyr Asn Ala Phe Asn Arg Phe Leu His Ala  
 210 215 220

20

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

30 Met Lys Xaa  
 1

35 (2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Met Gln Ala Pro Phe Xaa His Phe Ser Phe Arg Met Phe Ser Asn Leu  
 1 5 10 15

45 Tyr Cys Phe Ser Asp Phe Gln Pro Asn Ile Ser Pro Cys Pro Leu Cys  
 20 25 30

50 His Cys Ile Leu Pro Xaa His His His Val Phe Leu Leu Leu Ala Val  
 35 40 45

Xaa

55

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 amino acids

60

508

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

5 Met Lys Leu Val Thr Met Phe Asp Lys Leu Ser Arg Asn Arg Val Ile  
 1 5 10 15  
 Gln Pro Met Gly Met Ser Pro Arg Gly His Leu Thr Ser Leu Gln Asp  
 20 25 30  
 10 Ala Met Cys Glu Thr Met Glu Gln Gln Leu Ser Ser Asp Pro Asp Ser  
 35 40 45  
 15 Asp Pro Asp Xaa  
 50

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

20 Met Ala Val Gly Glu Ala Val Phe Val Pro Leu Gln His Pro Pro Leu  
 1 5 10 15  
 30 Leu His Gly Ser Pro Ile Pro Lys Leu Leu Pro Gly Pro Leu Leu Xaa  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

40 Met Asn Gly Cys His Arg Arg Lys Arg Leu His Leu Cys Lys Thr Ile  
 1 5 10 15  
 50 Tyr Leu Leu Trp Phe Val Phe Ser Phe Leu Leu Ser Asn Glu Val Val  
 20 25 30  
 Ser Ser His Trp His Ile Leu Arg Ala Val Gln Ile Ile Cys Thr Leu  
 35 40 45  
 55 Phe His Arg Xaa Ile Ser Ala Phe Xaa  
 50 55

60 (2) INFORMATION FOR SEQ ID NO: 274:

509

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

Met Gly Trp Val Ser Ser Pro His Val Lys Arg Arg Glu Cys Val Leu  
 1 5 10 15  
 Lys Lys Pro Phe Phe Xaa  
 20

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Met Phe Asn Phe Phe Lys Asn Pro Leu Leu Thr Cys Leu Phe Ile Ser  
 1 5 10 15  
 Cys Tyr Leu Tyr Leu Ser Leu Leu Val Asn Lys Val Leu Phe Ala Glu  
 20 25 30  
 Glu Gly Leu Cys Cys Thr Tyr Cys Thr Thr Ser Asn Thr Gly Glu Gly  
 35 40 45  
 Gly Val Xaa  
 50

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Met Xaa  
 1

## (2) INFORMATION FOR SEQ ID NO: 277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

Met Leu Cys Thr Ile Leu Thr Val Val Ile Ile Ala Ala Gln Thr  
 1 5 10 15

510

Thr Arg Thr Thr Gly Ile Pro Lys Asn Ala Pro Gly Pro Ala Pro Leu  
 20 25 30

5 Cys Ala Pro Arg Ser Pro Arg Leu Phe Leu Gln Xaa Tyr Arg Gly Pro  
 35 40 45

Asn Gly Arg Pro Ala His Pro Phe Leu Gly Pro Ser Asp Leu Asp Thr  
 50 55 60

10 Ser Xaa  
 65

15

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

25 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser Pro  
 1 5 10 15

Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly Trp Ala  
 20 25 30

30 Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val  
 35 40 45

Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu  
 50 55 60

35 Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Xaa Ala Val Arg Ser His  
 65 70 75 80

40 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Ser Gly Ala Ile  
 85 90 95

Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala  
 100 105 110

45 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe  
 115 120 125

50 His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met  
 130 135 140

Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val  
 145 150 155 160

55 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly  
 165 170 175

Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Xaa Ser Thr Gly Trp Leu  
 180 185 190

60 Glu Ile Leu Lys Phe Leu Trp Leu Pro His Leu Pro Ser Leu Lys Asp

511

195

200

205

Pro Ser Leu Ser Ser Thr Arg Ile Gln Pro Leu Thr Thr Phe Phe Cys  
 210 215 220

Pro Leu Leu Pro Xaa Lys Gln Xaa Lys Gln Xaa Xaa Xaa Ser Leu Trp  
 225 230 235 240

Leu Leu Ser His Leu Phe Ala Trp Glu Pro Val Pro Asn Thr Gln Val  
 245 250 255

Xaa

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

Met Ala Pro Arg Ala Leu Pro Gly Ser Ala Val Leu Ala Ala Ala Val  
 1 5 10 15

Phe Val Gly Gly Ala Val Ser Ser Pro Leu Val Ala Pro Asp Asn Gly  
 20 25 30

Ser Ser Arg Thr Leu His Ser Arg Thr Glu Thr Thr Pro Ser Pro Ser  
 35 40 45

Asn Asp Thr Gly Asn Gly His Pro Glu Tyr Ile Ala Tyr Ala Leu Val  
 50 55 60

Pro Val Phe Phe Ile Met Gly Leu Phe Gly Val Leu Ile Xaa Pro Xaa  
 65 70 75 80

Xaa Xaa Lys Lys Lys Gly Tyr Arg Cys Thr Thr Glu Ala Glu Gln Asp  
 85 90 95

Ile Glu Glu Glu Lys Gly Xaa  
 100

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Met Pro Val Thr Leu Ser Ser Leu Gly Phe Trp Val Leu Leu Ser Leu  
 1 5 10 15

Leu Phe Pro Trp Arg Thr Asp Gln Gly Cys Gly Pro Ala Thr Cys Tyr  
 20 25 30

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

15 Met Val Leu Gly Leu Leu Leu Leu Xaa Phe Phe Ser Phe Ser Ser  
 1 5 10 15  
 Ser Pro Ser Pro Ser Ser Ser Leu Leu Leu Ser Ser Phe Phe Phe  
 20 25 30  
 Gln Ser Leu Ala Leu Ser Pro Arg Leu Glu Xaa  
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

35 Glu Trp Leu Val Phe Thr Phe Leu Leu Val Phe Gly Ser Pro Leu Gly  
 1 5 10 15  
 Lys Gly Pro Leu Xaa  
 20

40

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

50 Met Ile Arg Ala Leu Ser Leu Phe Leu Leu Ile Phe Asp Ala Ala Leu  
 1 5 10 15  
 Phe Ser Leu Ser Val Phe Val Phe Ile Gly His Leu Leu Pro Met Pro  
 20 25 30  
 Lys Gly Thr Gly Leu His Ser Cys Ala Lys His Leu Ile Lys Ser Leu  
 35 40 45  
 Lys Glu Asn Val Leu Pro Leu Met Asn Tyr Pro Asp Cys Lys Leu Lys  
 60 50 55 60

Ile Asn Ile Ser Pro Xaa  
65 70

5

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

15 Met Gly Lys Leu Ile Arg Leu Ser Val Met Val Met Ser Val Arg Arg  
1 5 10 15  
20 Leu Phe Ser Ile Tyr Trp Val Leu Ser Thr Val Pro Asp Ala Val Gly  
20 25 30  
Ser Arg Gly Gly Met Glu Glu Glu Cys Ser Arg Gly Leu Cys Cys Val  
35 40 45  
25 Ala Gly Gln His Lys Gln Ala Lys Gly Lys Arg Gln Ala Trp Asn Lys  
50 55 60  
Gly Gly Glu Tyr Gln Cys Val Thr Tyr Cys Xaa  
65 70 75

30

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

40 Met Pro Ala Leu Val Thr Leu Leu Leu Leu Phe Pro Leu Leu Pro Leu  
1 5 10 15  
Met Glu Ala Ser Cys His Val Met Arg Cys Pro Met Glu Arg Pro Thr  
20 25 30  
45 Xaa

50

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

60 Glu Ala Pro Trp Gly Leu Leu Lys Leu Leu Leu Leu Ala Val Phe  
1 5 10 15

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

15 Met Gln Gln Lys Gln Lys Lys Ala Asn Glu Lys Lys Glu Glu Pro Lys  
1 5 10 15

Xaa

20

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

30

Met Gln Arg Lys Val Ser Asp Phe Ile Ile His-Gln Arg Leu Thr Val  
1 5 10 15

35

Asn Leu Cys Val Ile Ser Phe Phe Phe Phe Leu Pro Ile Cys Ile Phe  
20 25 30

Ser Leu Ala Lys Lys Xaa  
35

40

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

50

Met Ala Leu Leu Ile Ser Ser Leu Ile Trp Ser Xaa  
1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60



515

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

Met Gln Met Phe Thr Val Ser Leu Leu Leu Ser Leu Leu Leu Arg Ser  
 1 5 10 15  
 Thr Asp Gln Asn His Leu Gln Leu Leu Val Gly Arg Glu Asp His Tyr  
 20 25 30  
 Gly Gly Xaa  
 35

## (2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

Met Ser Glu Ser Ala Cys Ile Leu Asn Asn Gln Lys Glu Leu Xaa  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

Met Asp Leu Asp Arg Val Lys Ala Glu Ala Thr Glu Asp Ile Thr Ser  
 1 5 10 15  
 Gly Val Leu Cys Leu Leu Phe Leu Arg Leu Pro Pro Asn Ser Cys Ile  
 20 25 30  
 Phe Pro Ser Ala Val Leu Gly Ser Thr Arg Thr Xaa  
 35 40

## (2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 136 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu  
 1 5 10 15  
 Leu Leu Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr  
 20 25 30  
 Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val

516

35                      40                      45  
 Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys  
     50                      55                      60  
 5  
 Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu  
     65                      70                      75                      80  
 Ala Leu Phe Ala Ser Gly Leu Ile His Arg Val Cys Val Thr Thr Cys  
                     85                      90                      95  
 10  
 Phe Ile Phe Ser Met Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser  
                     100                      105                      110  
 15  
 Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala Lys Val Thr  
                     115                      120                      125  
 Gly Lys Ser Lys Lys Arg Asn Xaa  
     130                      135  
 20

(2) INFORMATION FOR SEQ ID NO: 294:

- 25            (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 34 amino acids  
               (B) TYPE: amino acid  
               (D) TOPOLOGY: linear  
 30            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu  
     1                      5                      10                      15  
 35  
 Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys Leu  
                     20                      25                      30  
 Arg Xaa

40

(2) INFORMATION FOR SEQ ID NO: 295:

- 45            (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 137 amino acids  
               (B) TYPE: amino acid  
               (D) TOPOLOGY: linear  
 50            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Arg Thr Pro Gly Pro Leu Pro Val Leu Leu Leu Leu Ala Gly  
     1                      5                      10                      15  
 Ala Pro Ala Ala Arg Pro Thr Pro Pro Thr Cys Tyr Ser Arg Met Arg  
                     20                      25                      30  
 55  
 Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu Gln Val Ser  
                     35                      40                      45  
 60  
 Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg Leu Tyr Leu Asp  
     50                      55                      60

517

Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg Asp Phe Val Ala Ser  
65 70 75 80

5 Pro Pro Cys Trp Lys Val Ala Gln Val Asp Ser Leu Lys Asp Lys Ala  
85 90 95

Arg Lys Leu Tyr Thr Ile Met Asn Ser Phe Cys Arg Arg Asp Leu Val  
100 105 110

10 Phe Leu Leu Asp Asp Cys Asn Ala Leu Glu Tyr Pro Ile Pro Val Thr  
115 120 125

15 Thr Val Leu Pro Asp Arg Gln Arg Xaa  
130 135

(2) INFORMATION FOR SEQ ID NO: 296:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Trp Leu Leu Lys Pro Ser Ala His Ser Pro Val His Xaa Leu Val  
1 5 10 15

30 Leu Leu Phe Pro Arg Gly Trp Ser Gln Pro Gly Thr His Lys Arg Gln  
20 25 30

Ile Leu Val Asn Xaa Ala Ser Leu Pro Gly Gly Cys Leu Leu Pro Trp  
35 40 45

35

Ile Trp Ser Gly Ala Ala Leu Arg Phe Xaa  
50 55

40

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

45

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Ser Arg Arg Ala Glu Ala Ser Ile Phe Val Leu Pro Lys Thr Leu  
50 1 5 10 15

Leu Phe Val Leu Phe Pro Ala Phe Pro Ser Pro Ala Val Gly Cys Pro  
20 25 30

55

Val Pro Xaa  
35

60

(2) INFORMATION FOR SEQ ID NO: 298:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Ser Cys Tyr Ile Thr Pro Trp Ser Lys Ile Gln Ser Phe Ser Leu Ser  
 1 5 10 15  
 Leu Phe Gln Phe Ile Leu Gln Glu Val Asn Ile Thr Leu Pro Glu Asn  
 20 25 30  
 Ser Val Trp Tyr Glu Arg Tyr Lys Phe Asp Ile Pro Val Phe His Leu  
 35 40 45  
 Asn Gly Gln Phe Leu Met Met His Arg Val Asn Thr Ser Lys Leu Glu  
 50 55 60  
 Lys Gln Leu Leu Lys Leu Glu Gln Gln Ser Thr Gly Xaa Xaa  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

Met Phe Val Leu Phe Ser Leu Pro Lys Tyr Ala Gly Leu Arg Leu Pro  
 1 5 10 15  
 Ile Pro Gly Leu Ser Ala Leu Leu Val Phe Leu Leu Ser Leu Phe Ser  
 20 25 30  
 Arg Arg Ala Gln Val Glu Leu Thr Thr Gly Arg Glu Thr Leu Pro Lys  
 35 40 45  
 Asn Leu Gln Gly Tyr Phe Pro Glu Phe Gly Phe Gln Val Gln Asn Phe  
 50 55 60  
 Leu Ser Cys Lys Ile Tyr Ala Ala Ser Gln Lys Gln Pro Leu Pro Pro  
 65 70 75 80  
 Leu Tyr Gln Leu Arg Phe Tyr Leu Lys His Met Gly Leu Pro Xaa  
 85 90 95

## (2) INFORMATION FOR SEQ ID NO: 300:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

519

Met Ser Ser His Trp Thr Leu Lys Ile Leu Leu Val Pro Leu Phe Tyr  
1 5 10 15

Leu Ser Leu Glu Phe Pro Ser Gly Phe Val Leu Cys Leu Ala Asn Asp  
5 20 25 30

Leu Gly Tyr His Phe Ser Ser Arg Val Arg Ser Xaa  
35 40

10

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 31 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

20 Met Leu Val Val Asn Ile Asn Leu Val Phe Leu Leu Phe Phe Ile Phe  
1 5 10 15

Leu Cys Tyr Leu Asp Ala Cys Ile Asn Val Phe Cys Phe Tyr Xaa  
20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

35 Met Pro Val Leu Pro Gly Arg Thr Thr Ala Leu Leu Ser Leu Thr Leu  
1 5 10 15

40 Ala Phe Ala Val Pro Cys Ser Gly Val Glu Ala Gly Pro Cys Val Pro  
20 25 30

Arg Ser His Gly Cys Ser Ser Trp Glu Ala Ser Val Cys Val Thr Ser  
35 40 45

45 Ser Thr Pro Gly Gly Ser Trp Arg Ala Arg Ala Leu Phe Pro Ser Ala  
50 55 60

Ala Trp His Arg Xaa Ala Ala Trp Asp Ser Pro Trp Thr Gln Thr Gly  
65 70 75 80

50

Asp Phe Ala Arg Gly Ala Met Gly Gly Ala Gly Ala Leu Pro Gly Gly  
85 90 95

55 Cys Val Cys Ile Ser Gly Arg Pro Arg Ala Gln Lys Leu Pro Ala Leu  
100 105 110

Xaa

60

520

## (2) INFORMATION FOR SEQ ID NO: 303:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

10 Thr His Ile His Thr His Ile Ile Ile Cys Ser Ser Val Xaa  
1 5 10

## 15 (2) INFORMATION FOR SEQ ID NO: 304:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

25 Met Glu Asn Phe Phe Phe Ser Phe Tyr Leu Phe Leu Ile Thr Leu Ile  
1 5 10 15

Pro Asn Gly Arg Thr Leu Ser Thr Thr Ala Asp His Cys Lys Ile Pro  
20 25 30

30 Cys Ile Xaa  
35

## 35 (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

40 Met Glu Leu Trp Glu Leu Ala Leu Cys Leu Leu Val Ala Leu Ser Ala  
1 5 10 15

45 His Met Phe Thr Val Gln Leu Leu Ala Asp Leu Gly Phe Leu Phe Gly  
20 25 30

50 Gly Phe Xaa  
35

## (2) INFORMATION FOR SEQ ID NO: 306:

## 55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

60



## 5 (2) INFORMATION FOR SEQ ID NO: 309:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Gln Val Val Gly Ser Trp Pro Gly Arg Val Gly Val Val Gly Leu  
 1 5 10 15  
 Ala Phe Ser Leu Val Ile Pro Pro Pro Ala Ile Cys Ile Ala Gly Pro  
 20 25 30  
 Ala Pro Gly Leu Gly Gly Gly Glu Arg Gln Gln Lys Gly Leu Gly Arg  
 35 40 45  
 Gly Gly Gly Gly Leu Arg Asn Cys Pro Gly Arg Val Gly Met Ala Ala  
 50 55 60  
 Glu Pro Gly Ala Leu Leu Cys Leu Thr Ser Arg Asp Gly Ser Leu Leu  
 65 70 75 80  
 Leu Ser Cys Val Arg Pro His His Val Ile Lys Pro Lys Gly Thr Ala  
 85 90 95  
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Xaa Xaa  
 100 105 110  
 Gly Gly Xaa  
 115

35

## 40 (2) INFORMATION FOR SEQ ID NO: 310:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

Met Asp Leu Pro Gln Phe Ile Tyr Leu Phe Ile Phe Cys Phe Cys Cys  
 1 5 10 15  
 Leu Ala Ile Val Asn Asn Ala Ser Ile Asn Ile His Ile Gln Val Ser  
 20 25 30  
 Met Trp Leu Tyr Val Phe Ile Ser Leu Gly Tyr Leu His Gly Ser Arg  
 35 40 45  
 Ile Leu Gly His Asn Ile Ile Leu Cys Leu Thr Ser Gln Arg Ile Ala  
 50 55 60  
 Lys Arg Phe Phe Ile Val Ala Ala Ser Phe Thr Phe Pro Pro Ala Met  
 65 70 75 80

60



523

Tyr Lys Asp Phe Tyr Phe Ser Ile Ser Leu His Leu Pro Thr Leu Leu  
85 90 95

5 Phe Xaa Xaa Xaa Phe Val Phe Ser Leu Leu Pro Pro  
100 105

10 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Cys Ser Pro Ser Leu Ser Ser Ser Pro Pro Pro Leu Leu Gln Val  
1 5 10 15

20

Phe Phe Phe Phe Phe Ser Pro His Trp Ala Ala Lys Val Val Pro  
20 25 30

25

Gln Trp Lys Xaa Arg His Pro Gln Val Ser Ser Gln Leu Leu Leu Cys  
35 40 45

Phe Leu Arg Val Asn Cys Gln Phe Leu Phe Leu Gln Glu Ile Leu Phe  
50 55 60

30

Xaa  
65

35 (2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Cys Leu Ser Arg Trp Lys Ile Phe Tyr Thr Leu Leu Ile Leu Phe  
1 5 10 15

45

Xaa Xaa Phe Ser Ile Thr Ser Glu Xaa Glu Thr Phe Tyr Met Ile Ile  
20 25 30

50

Ile His His Asn Pro Thr Gln Ile Thr Ala Ser Cys Ser Phe Thr Phe  
35 40 45

Leu Xaa  
50

55

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

60

524

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

5 Met Glu Arg Pro Asp Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser  
 1 5 10 15  
 Leu Pro Ala Gly Ser Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr  
 20 25 30  
 10 Ala Gly Tyr Xaa Gln Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr  
 35 40 45  
 Leu Leu Leu Cys Arg Arg Leu Leu Ser Pro Met Asn Leu Leu Ser Leu  
 15 50 55 60  
 His Thr Ala Ser Gly Leu Arg Leu Phe Ser Val Leu Ser Leu Ala Trp  
 65 70 75 80  
 20 Gly Phe Ile Ala Asp Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu  
 85 90 95  
 Gly Glu Met Arg Phe Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu  
 100 105 110  
 25 Arg Thr Tyr Arg Gly Arg Leu Ala Tyr Leu Pro Val Gly Arg Val Gly  
 115 120 125  
 Ser Lys Thr Pro Ala Ser Pro Val Val Val Gln Gln Gly Pro Val Asp  
 30 130 135 140  
 Ala His Leu Val Pro Leu Glu Glu Pro Val Pro Ser His Trp Thr Val  
 145 150 155 160  
 35 Val Pro Asp Glu Asp Phe Val Leu Val Leu Ala Leu Leu His Ser His  
 165 170 175  
 Leu Gly Ser Glu Met Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly  
 180 185 190  
 40 Val Met His Leu Phe Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu  
 195 200 205  
 Leu Arg Leu Phe Leu Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu  
 45 210 215 220  
 Cys Pro Tyr Leu Val Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro  
 225 230 235 240  
 50 Lys Asp Gly Lys Gly Val Phe Ala Val Asp Gly Glu Leu Met Val Ser  
 245 250 255  
 Glu Ala Val Gln Gly Gln Val His Pro Asn Tyr Phe Trp Met Val Ser  
 260 265 270  
 55 Gly Cys Val Glu Pro Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro  
 275 280 285  
 60 Pro Glu Glu Pro Leu  
 290

525

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Pro Leu Glu Gly Phe Cys Leu Val Leu Asp Ile Gly Phe Leu Leu  
 1 5 10 15  
 Val Met Leu Ile Ser Leu Ala Ser Glu Cys Phe Thr Thr Cys Leu Asp  
 20 25 30  
 Ser Phe Ser Thr Thr Glu Pro Gly Cys Lys Phe Tyr Lys Leu Leu His  
 35 40 45  
 Ser Val Ser Leu Leu Asn Ile Asn Phe Asn Val Lys Ser Leu Leu Cys  
 50 55 60  
 Ser His Ile Xaa  
 65

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Met Pro Leu Gln Leu Ser Gly Gln Tyr Trp Ile Ser Leu Leu Val Phe  
 1 5 10 15  
 Leu Ser Leu Gln Pro Phe Pro Gln Ala Ala Ile Pro Cys Ala Leu Thr  
 20 25 30  
 Asp Val Gly Gly Ser Cys Val Ile Cys His Ile Leu Leu Asn Cys Leu  
 35 40 45  
 Cys Ile Leu Phe Thr Leu Thr Ala Pro Ser Leu Ser His Val Leu Leu  
 50 55 60  
 Ile Lys Met Ser Leu Ser Val Cys Tyr Glu Pro Gly Ala Asp Leu Ser  
 65 70 75 80  
 Asp Arg Ala Ala Thr Gly Asn Lys Lys Leu Thr Arg Ser Thr Cys Leu  
 85 90 95  
 Leu Met His Ser Asn Lys Leu Cys Xaa  
 100 105

## (2) INFORMATION FOR SEQ ID NO: 316:

526

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Trp Gly Cys Ser Gly Leu Gly His Arg Thr Val Ser Phe Leu Leu  
 1 5 10 15  
 Leu Leu Pro Cys Ser Phe Pro Arg Pro Cys Xaa Leu Phe Gly Leu Ile  
 20 25 30  
 Pro Ile Ser Arg Pro Cys Lys Val Glu Ala Pro Arg Leu Ser Val Pro  
 35 40 45  
 Xaa Leu Ser Cys Ala Ser His Pro Tyr Cys Asn Cys Pro Met Ser Thr  
 50 55 60  
 Ser Cys Pro Leu Pro Arg Xaa  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 317:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Leu Asn Val Leu Ser Lys Val Gln Gln Leu Val Ser Xaa Leu Gly  
 1 5 10 15  
 Leu Val Thr Phe Leu Leu Asn His Ser Ala Ala Gly Gly Ser Pro Gln  
 20 25 30  
 His Arg Trp Leu Leu Leu Xaa  
 35

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Lys Ala Ile Ala Arg Ala Cys Leu Leu Leu Ser Leu Leu Val Leu  
 1 5 10 15  
 Pro His Val Val Ser Glu His Leu Phe Trp His His Asn Pro Arg His  
 20 25 30  
 Pro Val Ile Trp Pro Phe Pro Pro Phe His Leu Ile Ser Cys Ser Val  
 35 40 45

527

Ser Ala Ser Thr Trp His Leu Gly Glu Xaa Leu Leu Leu Val Pro  
50 55 60

Ile Ala Pro Ser Val Trp Ser Xaa  
5 65 70

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Glu Gln Gly Gly Gly Pro Arg Leu Leu Leu Ile Pro Gly Leu  
1 5 10 15

Leu His Asn Thr Tyr Leu Ala Arg Pro Gly Asp Phe Pro Ala Gln Gly  
20 25 30

Thr Thr Glu Asn Thr Glu Cys Gln Gly Ser Pro Ser Pro Ile Ser His  
35 40 45

Leu Gly Lys Val Arg Ser Leu Asp Ser Asn Thr Gln Ile Xaa  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Pro Leu Leu Phe Phe Ser Val Ser Thr Leu Phe Ser Gly Ser Val  
1 5 10 15

Thr Leu Gln Gln Arg Gly Met Phe Leu Pro Trp Thr Gly Thr Gly Glu  
20 25 30

Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu Met  
35 40 45

Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly Leu  
50 55 60

Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser Ser  
65 70 75 80

Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met Gln  
85 90 95

Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg Val  
100 105 110

Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile Asn

528

115 120 125

Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp Asp  
130 135 140

5 Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr Gln  
145 150 155 160

10 Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val Ala  
165 170 175

Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu Arg  
180 185 190

15 Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe Gly  
195 200 205

Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met Arg  
210 215 220

20 Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser Ile Ile Gln Gly Ala Leu  
225 230 235 240

Thr Gln Leu Ile Gln Leu Tyr His Arg Phe His Arg Val Leu Ser Gln  
245 250 255

Pro Gln Leu Arg Ala Leu Pro Ala Arg Ala Glu Leu Ile Asn Ile His  
260 265 270

30 His Leu Met Val Glu Leu Lys Lys His Lys Pro Asn Phe Xaa  
275 280 285

35 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Phe Arg Ala Leu Arg Asp Leu Leu Thr His Tyr Pro Gln Gln Ile  
1 5 10 15

45 Leu Leu Gln Val Leu Val Val Met Tyr Gln Val Leu Gln Val Trp Glu  
20 25 30

Leu Pro Trp Pro Glu Leu Ile His Leu Gln Gly Ile Val Pro Thr Asp  
35 40 45

Gln Leu His Leu Lys Gln Xaa  
50 55

55

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

60

529

(2) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

5 Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn Pro Pro  
 1 5 10 15  
 Cys Leu Leu Ser Thr Val Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys  
 20 25 30  
 10 Leu Ser Gly Glu Glu Ser Tyr Trp Trp Met Gln Phe Thr Ala Ala Val  
 35 40 45  
 15 Glu Phe Ile Lys Thr Ile Asp Asp Arg Lys Xaa  
 50 55

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

20 Met His Pro Ala Arg Lys Leu Leu Ser Leu Leu Phe Leu Ile Leu Met  
 1 5 10 15  
 30 Gly Thr Glu Leu Thr Gln Asp Ser Ala Ala Pro Asp Ser Leu Leu Arg  
 20 25 30  
 Ser Ser Lys Gly Ser Thr Arg Gly Ser Leu Ala Ala Ile Val Ile Trp  
 35 40 45  
 Arg Gly Lys Ser Glu Ser Arg Ile Ala Lys Thr Pro Gly Ile Phe Arg  
 50 55 60  
 40 Gly Gly Gly Thr Leu Val Leu Pro Pro Thr His Thr Pro Glu Trp Leu  
 65 70 75 80  
 Ile Leu Pro Leu Gly Ile Thr Leu Pro Leu Gly Ala Pro Glu Thr Gly  
 85 90 95  
 45 Gly Gly Asp Cys Ala Ala Glu Thr Trp Lys Gly Ser Gln Arg Ala Gly  
 100 105 110  
 Gln Leu Cys Ala Leu Leu Ala Xaa  
 115 120  
 50

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

60

530

Phe Phe Leu Val Val Phe Ser Leu Ser Phe Xaa Pro Ser Val Leu Thr  
 1 5 10 15  
 Ser Pro Val His Xaa Pro His Cys Cys Gln Xaa Asp Xaa Ile Leu Phe  
 5 20 25 30  
 Lys Asn Thr Leu Xaa Xaa Phe Xaa Ala Lys Tyr Xaa  
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

15

20

Met Phe Ser Arg Thr Ser Asn Phe Trp Thr Phe Phe Phe Gln Phe Leu  
 1 5 10 15

Ile Phe Lys Val Phe Leu Val Leu Lys Asn Xaa Phe Thr Ser Gln Lys  
 20 25 30

25

Ile Xaa Xaa Ile Xaa Xaa Glu Lys Pro Lys Lys Lys Lys Xaa Arg Gly  
 35 40 45

30

Gly Arg Ala Pro Ser Pro Gln Gly Gly Pro Xaa  
 50 55

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

35

40

Met Gly Leu Leu Ile Phe Met Leu Leu Ile Gly Ile His Ser Gln Cys  
 1 5 10 15

45

Ser Xaa

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

50

55

Met Val Leu Phe Cys Phe Val Leu Phe Cys Phe Val Phe Glu Met Asp  
 1 5 10 15

60



531

Ser Ser Ser Val Thr Gln Ala Gly Val Gln Trp Cys Asp Leu Gly Ser  
 20 25 30

5 Leu Gln Ala Pro Pro Pro Gly Phe Ser Pro Phe Ser Cys Leu Ser Leu  
 35 40 45

Pro Ser Ser Trp Asp Tyr Arg Arg Pro Pro Pro Arg Pro Ala Asn Phe  
 50 55 60

10 Leu Tyr Phe Leu Val Glu Thr Gly Phe His His Val Ser Gln Asp Gly  
 65 70 75 80

Leu Asp Leu Leu Thr Ser Xaa  
 85

15

(2) INFORMATION FOR SEQ ID NO: 328:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 538 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

25 Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile Leu Leu Val Phe  
 1 5 10 15

30 Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala Pro Gly Pro Thr  
 20 25 30

Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp Ala Arg Lys Asn  
 35 40 45

35 His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro Asn His Cys Asp  
 50 55 60

Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu Ile Glu Ala Asn  
 65 70 75 80

40 Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His Met Glu Met Ser  
 85 90 95

45 Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe  
 100 105 110

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val  
 115 120 125

50 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala  
 130 135 140

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys  
 145 150 155 160

55 Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe  
 165 170 175

60 Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg  
 180 185 190

532

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile  
 195 200 205  
 5 Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys  
 210 215 220  
 Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile  
 225 230 235 240  
 10 Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val  
 245 250 255  
 Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile  
 15 260 265 270  
 Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met  
 275 280 285  
 20 Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu  
 290 295 300  
 Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu  
 305 310 315 320  
 25 Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val  
 325 330 335  
 Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln  
 340 345 350  
 30 Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu  
 355 360 365  
 35 Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr  
 370 375 380  
 Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser  
 385 390 395 400  
 40 Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His  
 405 410 415  
 Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu  
 420 425 430  
 45 Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr  
 435 440 445  
 50 Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala  
 450 455 460  
 Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu  
 465 470 475 480  
 55 Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser  
 485 490 495  
 60 Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe  
 500 505 510

533

Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe  
515 520 525

5 Ile Asn Asp Asn Ala Ala Ser Gly Ile Xaa  
530 535

10 (2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Gly Ile Ala Leu Ala Val Leu Gly Trp Leu Ala Val Met Leu Cys  
1 5 10 15

20 Cys Ala Leu Pro Met Trp Arg Val Thr Ala Phe Ile Gly Ser Asn Ile  
20 25 30

25 Val Thr Ser Gln Thr Ile Trp Glu Gly Leu Trp Met Asn Cys Val Val  
35 40 45

Gln Ser Thr Gly Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala  
50 55 60

30 Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala Leu Val Ile Ile Ser Ile  
65 70 75 80

Ile Val Ala Ala Leu Gly Val Leu Leu Ser Val Val Gly Gly Lys Cys  
85 90 95

35 Thr Asn Cys Leu Glu Asp Glu Ser Ala Lys Ala Lys Thr Met Ile Val  
100 105 110

40 Ala Gly Val Val Phe Leu Leu Ala Gly Leu Met Val Ile Val Pro Val  
115 120 125

Ser Trp Thr Ala His Asn Ile Ile Gln Asp Phe Tyr Asn Pro Leu Val  
130 135 140

45 Ala Ser Gly Gln Lys Arg Glu Met Gly Ala Ser Leu Tyr Val Gly Trp  
145 150 155 160

Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu Leu Cys Cys Asn  
165 170 175

50 Cys Pro Pro Arg Thr Asp Lys Pro Tyr Ser Ala Lys Tyr Ser Ala Ala  
180 185 190

55 Arg Ser Ala Ala Ala Ser Asn Tyr Val Xaa  
195 200

60 (2) INFORMATION FOR SEQ ID NO: 330:

534

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Ala Thr Val Thr Ala Thr Thr Lys Val Pro Glu Ile Arg Asp Val  
 1 5 10 15  
 10 Thr Arg Ile Glu Arg Ile Gly Ala His Ser His Ile Arg Gly Leu Gly  
 20 25 30  
 Leu Asp Asp Ala Leu Glu Pro Arg Gln Ala Ser Gln Gly Met Val Gly  
 35 40 45  
 15 Gln Leu Ala Ala Arg Arg Ala Ala Gly Val Val Leu Glu Met Ile Arg  
 50 55 60  
 Glu Gly Lys Ile Ala Gly Arg Ala Val Leu Ile Ala Gly Gln Pro Gly  
 65 70 75 80  
 Thr Gly Lys Thr Ala Ile Ala Met Gly Met Ala Gln Ala Leu Gly Pro  
 85 90 95  
 25 Asp Thr Pro Phe Thr Ala Ile Ala Gly Ser Glu Ile Phe Ser Leu Glu  
 100 105 110  
 Met Ser Lys Thr Glu Ala Leu Thr Gln Ala Phe Arg Arg Ser Ile Gly  
 115 120 125  
 30 Val Arg Ile Lys Glu Glu Thr Glu Ile Ile Glu Gly Glu Val Val Glu  
 130 135 140  
 Ile Gln Ile Asp Arg Pro Ala Thr Gly Thr Gly Ser Lys Val Gly Lys  
 145 150 155 160  
 Leu Thr Leu Lys Thr Thr Glu Met Glu Thr Ile Tyr Asp Leu Gly Thr  
 165 170 175  
 40 Lys Met Ile Xaa Ser Leu Thr Lys Asp Lys Val Gln Ala Gly Asp Val  
 180 185 190  
 Ile Thr Ile Asp Lys Ala Thr Gly Lys Ile Ser Lys Leu Gly Arg Ser  
 195 200 205  
 45 Phe Thr Arg Ala Arg Glu Leu Arg Arg Tyr Gly Leu Pro Asp Gln Val  
 210 215 220  
 Arg Ala Val Pro Arg Trp Gly Ala Pro Glu Thr Gln Gly Gly Gly Ala  
 225 230 235 240  
 His Arg Val Pro Ala Arg Asp Arg Arg His Gln Leu Ser His Pro Gly  
 245 250 255  
 55 Leu Pro Gly Ala Leu Leu Arg  
 260

## 60 (2) INFORMATION FOR SEQ ID NO: 331:

535

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile Leu Leu Gly  
 1 5 10 15  
 Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys Glu Lys Gly  
 20 25 30  
 Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr  
 35 40 45  
 Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg Thr Tyr Asn  
 50 55 60  
 Gln His Tyr Asn Asn Leu Arg Gly Ala Val Ser Gln Arg Leu Tyr  
 65 70 75 80  
 Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala  
 85 90 95  
 Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp  
 100 105 110  
 Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile Tyr Glu Leu  
 115 120 125  
 Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val Leu Glu Tyr Ala Thr  
 130 135 140  
 Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln Ala Gly Phe  
 145 150 155 160  
 Ser Gly Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu  
 165 170 175  
 Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn Cys Arg Leu  
 180 185 190  
 Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser Leu Ser Gln  
 195 200 205  
 Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys Glu Glu Val Thr Val  
 210 215 220  
 Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr Ser Thr Met Ser Gln  
 225 230 235 240  
 Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys Pro Leu Pro Leu Arg  
 245 250 255  
 Thr Asp Phe Ser  
 260

60

536

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Thr Pro Gln Lys Pro Ala Leu Ala Val Leu Leu Leu Glu Val Pro  
 1 5 10 15  
 Leu Leu Leu Thr Leu Ser Val Leu Lys Lys Arg Cys Leu Val Thr Cys  
 20 25 30  
 Glu Pro Thr Ser Arg Phe Val Ser Cys Asp Leu Pro Leu Ser Val Xaa  
 35 40 45

## (2) INFORMATION FOR SEQ ID NO: 333:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu  
 1 5 10 15  
 Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala  
 20 25 30  
 Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser  
 35 40 45  
 Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr  
 50 55 60  
 Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile  
 65 70 75 80  
 Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe  
 85 90 95  
 Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg  
 100 105 110  
 Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys  
 115 120 125  
 Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg  
 130 135 140  
 Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn  
 145 150 155 160

537

Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr  
 165 170 175  
 5 Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser  
 180 185 190  
 Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met  
 195 200 205  
 10 Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr  
 210 215 220  
 Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe  
 225 230 235 240  
 15 Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu  
 245 250 255  
 Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu  
 260 265 270  
 Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg Tyr Lys Gly Xaa  
 275 280 285  
 25 Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys  
 290 295 300  
 Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val Ser Leu Gly Tyr Gly  
 305 310 315 320  
 30 Ile Val Lys Pro Arg Leu Glu Ser Leu Phe Ile Arg Leu Xaa  
 325 330

35

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

45

Met Val Leu Xaa Val Val Thr Leu Gly Leu Ala Leu Phe Thr Leu Cys  
 1 5 10 15

Gly Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu Leu Ile Thr  
 20 25 30

50

Ala Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr Met Tyr Leu  
 35 40 45

Phe Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn Asp Pro Thr  
 50 55 60

55

Leu Ala Ile Thr Leu Ala Ala Ser Ala Gly Ser Ser Ser Ser Thr  
 65 70 75 80

60

Pro Ser Leu Arg Ser Thr Ala Pro Phe Cys Gln Pro Cys Arg Arg Thr  
 85 90 95

538

Arg Pro Thr Thr Ser Thr Arg Arg Ser Pro Gly Cys Gly Arg Arg Pro  
100 105 110

5 Ser Arg Arg Thr Cys Ser Cys Arg Gly Pro Ile Trp Arg Thr Arg Pro  
115 120 125

10 Ser Pro Trp Met Asn Thr Met Gln Leu Ser Glu Gln Gln Asp Phe Pro  
130 135 140

Thr Ala Ala Trp Glu Lys Asp Pro Val Ala Ala Trp Gly Lys Asp Pro  
145 150 155 160

15 Ala Leu Arg Leu Glu Ala Thr Cys Ile Ser Gln Leu Arg Trp Pro Ser  
165 170 175

Cys Ser Thr Val Gly Pro Ser Gln Leu Leu Arg Gln Val Thr Gln Glu  
180 185 190

20 Xaa Thr Phe Gly Glu Arg Leu Xaa  
195 200

25 (2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

35 Met Leu Leu His His Gln Leu Leu Ile Val Thr Leu His Leu Val Leu  
1 5 10 15

Leu Leu Ala Thr Leu Leu Val Xaa  
20

40 (2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

50 Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala Leu  
1 5 10 15

Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val Leu Gln  
20 25 30

55 Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu  
35 40 45

60 Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser Lys Ile Asn Glu  
50 55 60



539

Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe Gln Ile Asn Ser His  
65 70 75 80

Tyr Trp Cys Asn Xaa Tyr Lys Ser Tyr Ser Glu Asn Leu Cys His Val  
85 90 95

Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu Ala Gly Ile His Cys  
100 105 110

Ala Lys Arg Ile Val Ser Gly Ala Arg Gly Met Asn Asn Trp Val Arg  
115 120 125

Met Glu Xaa Cys Thr Val Gln Ala Gly His Ser Ser Thr Gly Xaa  
130 135 140

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Leu Val Ile Ala Gly Gly Ile Leu Ala Ala Leu Leu Leu Ile  
1 5 10 15

Val Val Val Leu Cys Leu Tyr Phe Lys Ile His Asn Ala Leu Lys Ala  
20 25 30

Ala Lys Glu Pro Glu Ala Val Ala Val Lys Asn His Asn Pro Asp Lys  
35 40 45

Val Trp Trp Ala Lys Asn Ser Gln Ala Lys Thr Ile Ala Thr Glu Ser  
50 55 60

Cys Pro Ala Leu Gln Cys Cys Glu Gly Tyr Arg Met Cys Ala Ser Phe  
65 70 75 80

Asp Ser Leu Pro Pro Cys Cys Cys Asp Ile Asn Glu Gly Leu Xaa  
85 90 95

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Leu Leu Lys Ser Asn Ile Leu Met Leu Asn Leu Phe Ala Ala Asn  
1 5 10 15

Val Gly Ala Asn Phe Ala Leu Thr Val Glu Lys Ile Gly Met Ile Leu  
20 25 30

Leu Asn Val Ser Gly Xaa

540

35

5 (2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala

1

5

10

15

15

Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Pro

20

25

30

Leu Leu His Asp Gly Glu Xaa

35

20

25 (2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Ser Asp Pro Leu Ala Ser Ala Ser Gln Asn Ala Gly Ile Val Ser Val

1

5

10

15

35

Gly Leu Cys Thr Arg Pro Gly Pro Gln Phe Lys Asn Ala Gln Pro Pro

20

25

30

Phe Pro Xaa Gln Lys Ala Pro Arg Cys Leu Trp Glu Asn Gln Pro Pro

35

40

45

40

Pro Trp Arg Lys Ala Trp Asp Leu Pro Ser His Leu Gly Arg Arg Gly

50

55

60

Ile Cys Gly Lys Ser Phe Xaa

65

70

45

50 (2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Tyr Val Met Ile Phe Lys Lys Glu Phe Ala Pro Ser Asp Glu Glu Leu

1

5

10

15

60

Asp Ser Tyr Arg Arg Gly Glu Glu Trp Asp Pro Gln Lys Ala Glu Glu

541

20 25 30

Lys Arg Asn Xaa Lys Glu Leu Ala Gln Arg Gln Xaa Gly Gly Gly Ser  
35 40 45

5 Pro Ala Gly Ala Cys Gly Gly Glu Pro Cys Gln Arg Leu Gln Gly Gln  
50 55 60

10 Val Gln Pro Pro His Arg Gln Gly Ser Ser Gln Arg Arg Ser Pro His  
65 70 75 80

Ala Thr Gly Gln Xaa  
85

15

(2) INFORMATION FOR SEQ ID NO: 342:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

25

Met Trp Asp Trp Asp Trp Ser Ala Pro Trp Ser Trp Pro Leu Trp Leu  
1 5 10 15

Ser Leu Ala Leu Val Cys Leu Ser Ala Gly Ala Lys Gly His Arg Ala  
20 25 30

30

Ser Glu Ala Gly His Ala Arg Ala Leu Thr Cys Glu Met Gly Ser Glu  
35 40 45

35

Phe Xaa Thr Ala Xaa Gly Leu Val Leu Gly Xaa Xaa Xaa Trp Thr Xaa  
50 55 60

Xaa Asn Gly Ser Ala Gly Pro Glu Arg Arg Gly Trp Arg Pro Ala Ala  
65 70 75 80

40

Phe Leu Ala Val Phe Leu Leu Gly Asp Xaa  
85 90

45

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

50

Met Phe Gly Pro Thr Phe His Ser Leu Val Leu Val Pro Pro Trp Pro  
1 5 10 15

55

Asn Leu Ser Leu Leu His Phe Thr Ser Pro Val Gly Gln His Ser Ser  
20 25 30

60

Phe Leu Pro Thr Ser Leu Arg Leu Xaa Lys Lys Lys Lys Lys Lys Lys  
35 40 45

5

(2) INFORMATION FOR SEQ ID NO: 344:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

15

Met Cys Ser Lys Asn Gly Phe Leu Leu Ala Trp Ser Trp Asn Ser Pro  
 1 5 10 15

Trp Leu Pro Gln Ala Ser Leu Ala His Gly Cys Trp Gly Arg Trp Met  
 20 25 30

20

Ser Asp Leu Val Gly Cys Ser Arg Glu Asn Lys Cys Ala Leu Arg Asp  
 35 40 45

25

His Ser Glu Arg Val Gln Gly Xaa  
 50 55

30

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Ser Pro Leu Xaa Phe Cys Val Val Leu Leu Leu Gln Ala Ala Arg Gly  
 1 5 10 15

40

Tyr Val Val Arg Lys Pro Ala Gln Ser Arg Leu Asp Asp Asp Pro Pro  
 20 25 30

Pro Ser Thr Leu Leu Lys Asp Tyr Gln Asn Val Pro Gly Ile Glu Lys  
 35 40 45

45

Val Asp Asp Val Val Lys Arg Leu Leu Ser Leu Glu Met Ala Asn Lys  
 50 55 60

50

Lys Glu Met Leu Lys Ile Lys Gln Glu Gln Phe Met Lys Lys Ile Val  
 65 70 75 80

Ala Asn Pro Glu Asp Thr Arg Ser Leu Glu Ala Arg Ile Ile Ala Leu  
 85 90 95

55

Ser Val Lys Ile Arg Ser Tyr Glu Glu His Leu Glu Lys His Arg Lys  
 100 105 110

Asp Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile Asp Gln Arg Lys  
 115 120 125

60

543

Lys Met Leu Lys Asn Leu Arg Asn Thr Asn Tyr Asp Val Phe Glu Lys  
130 135 140

5 Ile Cys Trp Gly Leu Gly Ile Glu Tyr Thr Phe Pro Pro Leu Tyr Tyr  
145 150 155 160

Arg Arg Ala His Arg Arg Phe Val Thr Lys Lys Ala Leu Cys Ile Arg  
165 170 175

10 Val Phe Gln Glu Thr Gln Lys Leu Lys Lys Arg Arg Arg Ala Leu Lys  
180 185 190

Ala Ala Ala Ala Ala Gln Lys Gln Ala Lys Arg Arg Asn Pro Asp Ser  
195 200 205

15 Pro Ala Lys Ala Ile Pro Lys Thr Leu Lys Asp Ser Gln Xaa  
210 215 220

20

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

30 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
1 5 10 15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
20 25 30

35 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
35 40 45

40 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Xaa  
50 55 60

45

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

55 Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly  
1 5 10 15

Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly  
20 25 30

60 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala

544

35

40

45

Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro  
50 55 60

5

Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala  
65 70 75 80

Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val  
85 90 95

10

Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Xaa His  
100 105 110

15

Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Xaa Xaa Glu Glu Lys  
115 120 125

Gln Ala Arg Lys Ala Gln Xaa Glu Ala Glu Glu Ala Glu Arg Glu Xaa  
130 135 140

20

Arg Lys Arg Leu Glu Ser Gln Arg Glu Xaa  
145 150

25

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

30

Met Gln Lys Cys Met Leu Ser Ala Leu Val Phe His Ile Gln Trp Ser  
1 5 10 15

35

Xaa

40

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

45

Met Leu Val Cys Ser Phe Leu Phe Leu Xaa  
1 5 10

50

55

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Val Ile Glu Leu Cys Val Ser Leu Arg Ser Leu Asn Phe Xaa  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Cys Glu Phe Xaa Xaa Xaa Ile Met Xaa Leu Ala Gly Tyr Phe Ala  
 1 5 10 15

Cys Xaa

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Val Gly Gly Tyr Val Ser Ser Phe Ser Phe Pro Pro Val Ser Ser  
 1 5 10 15

Ser Leu Leu Leu Pro Ala Ser Phe Ala Phe Pro Phe Leu Pro Gly Thr  
 20 25 30

Pro Cys Pro Phe Leu Tyr Phe Leu Pro Ser Pro Phe Ser Pro Leu Pro  
 35 40 45

Leu Ser Leu Thr Arg Ser Asn Ser Phe Leu Leu Asn Gly Xaa  
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Glu Lys Lys Ser Met Ser Val Ser Asp Ile Tyr Ala Leu Glu Ser Leu  
 1 5 10 15

Gly Arg Ser Leu Phe Thr Leu Asn Ser Met Cys Leu Pro Leu Ser Phe  
 20 25 30

Xaa

## 5 (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Gly Gly Ala Ser Arg Arg Val Glu Ser Gly Ala Trp Ala Tyr Leu  
 1 5 10 15  
 Ser Pro Leu Val Leu Arg Lys Glu Leu Glu Ser Leu Val Glu Asn Glu  
 20 25 30  
 Gly Ser Glu Val Leu Ala Leu Pro Glu Leu Pro Ser Ala His Pro Ile  
 35 40 45  
 Ile Phe Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser  
 50 55 60  
 Ile Leu Pro Gly Leu Val Leu Ala Ser Cys Asp Gly Pro Ser Lys Ser  
 65 70 75 80  
 Gln Ala Pro Ser Pro Trp Leu Thr Pro Asp Pro Ala Ser Val Gln Val  
 85 90 95  
 Arg Leu Leu Trp Asp Val Leu Thr Pro Asp Pro Asn Ser Cys Pro Pro  
 100 105 110  
 Leu Tyr Val Leu Trp Arg Val His Ser Gln Ile Pro Gln Arg Val Val  
 115 120 125  
 Trp Pro Gly Pro Val Pro Ala Ser Leu Ser Leu Ala Leu Leu Glu Ser  
 130 135 140  
 Val Leu Arg His Val Gly Leu Asn Glu Val His Lys Ala Val Gly Leu  
 145 150 155 160  
 Leu Leu Glu Thr Leu Gly Pro Pro Pro Thr Gly Leu His Leu Gln Arg  
 165 170 175  
 Gly Ile Tyr Arg Glu Ile Leu Phe Leu Thr Met Ala Ala Leu Gly Lys  
 180 185 190  
 Asp His Val Asp Ile Val Ala Phe Asp Lys Lys Tyr Lys Ser Ala Phe  
 195 200 205  
 Asn Lys Leu Ala Ser Ser Met Gly Lys Glu Glu Leu Arg His Arg Arg  
 210 215 220  
 Ala Gln Met Pro Thr Pro Lys Ala Ile Asp Cys Arg Lys Cys Phe Gly  
 225 230 235 240  
 Ala Pro Pro Glu Cys  
 245



## (2) INFORMATION FOR SEQ ID NO: 355:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Lys Phe Ser Leu Leu Phe Leu Pro Met Leu Leu Ile Leu Lys Pro  
 1 5 10 15

15

Asp Leu Phe His Ile Ser Ile Cys Thr Leu Ala Ala Cys Gly Leu Thr  
 20 25 30

Phe Pro Xaa  
 35

20

## (2) INFORMATION FOR SEQ ID NO: 356:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

30

Met Leu Phe Phe Phe Ile Leu His Leu Leu Ser Ile Met Ser Phe Leu  
 1 5 10 15

Ser Pro Asp Ile Met Xaa  
 20

35

## (2) INFORMATION FOR SEQ ID NO: 357:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

45

Met Phe Gly Leu Leu Val Glu Ser Gln Thr Leu Leu Glu Glu Asn Ala  
 1 5 10 15

50

Val Gln Gly Thr Glu Arg Thr Leu Gly Leu Asn Ile Ala Pro Phe Ile  
 20 25 30

Asn Gln Phe Gln Val Pro Ile Arg Val Phe Leu Asp Leu Ser Ser Leu  
 35 40 45

55

Pro Cys Ile Pro Leu Ser Lys Pro Val Glu Leu Leu Arg Leu Asp Leu  
 50 55 60

60

Met Thr Pro Tyr Leu Asn Thr Ser Asn Arg Glu Val Lys Val Tyr Val  
 65 70 75 80

548

Cys Xaa Ile Trp Glu Asp Leu Thr Ala Ile Pro Phe Trp Val Ser Tyr  
85 90 95

Val Pro

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Gly Ala His Arg Xaa Trp Gln Gly Ser Val Leu Leu Phe Leu  
1 5 10 15

Ser Phe Ala Trp Gly Asn Gly Gly Ser Val Thr Phe Ser Asp Val Pro  
20 25 30

Arg Val Met Pro Leu Ala Gly Gly Pro Xaa Xaa Gln Val Ser Ser Thr  
35 40 45

Pro Arg Pro Pro Pro His Gln Val Thr Ser Ser Pro Gly Leu Glu Ser  
50 55 60

Ala His Ile Val Cys Pro Glu Arg Lys Lys Lys Lys Lys Lys  
65 70 75

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Thr Leu Leu Xaa Phe Leu Xaa Leu Leu Thr Thr Glu Gly Gly Arg Glu  
1 5 10 15

Asn Ile Phe Xaa Gly Arg Ile Leu Xaa Leu Gln Xaa Ser Pro Xaa  
20 25 30

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Leu Ser Phe Phe Ile Cys Leu Leu Ile Phe Val His Leu Leu Leu  
1 5 10 15

Leu Ser Phe Leu Ile Ser Asp Trp Pro Pro Pro Thr Gly Ser Ala Xaa  
                   20                                  25                                  30

5 His Lys Ile Leu Arg Leu Met Val Val Gln Arg Leu Ser Leu Leu Asp  
                   35                                  40                                  45

Gln Arg Lys Arg Trp Ser Glu Ala Xaa  
           50                                  55

10

(2) INFORMATION FOR SEQ ID NO: 361:

15 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 3 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

20 Lys Tyr Xaa  
      1

25 (2) INFORMATION FOR SEQ ID NO: 362:

      (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 32 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

35 Trp Ser Ser Ala Ser Ser Ser Trp Val Thr Thr Pro Glu Arg Ile Arg  
      1                                  5                                  10                                  15  
 Pro Arg Met Asp Thr Leu Pro Val Lys Gly His Phe Leu Ser Met Xaa  
           20                                  25                                  30

40

45 (2) INFORMATION FOR SEQ ID NO: 363:

      (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 28 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

50 Asp Ile Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile  
      1                                  5                                  10                                  15  
 55 Asn Leu Thr Ala Xaa Asp Thr Val His Phe Leu Xaa  
           20                                  25

60 (2) INFORMATION FOR SEQ ID NO: 364:

550

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Thr Leu Thr Ser Phe Leu Glu Leu Pro Leu Ala Pro Glu Pro Xaa  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met His Arg Tyr Ile Thr Phe Phe Lys Cys Phe Arg Ser Val Ile Leu  
 1 5 10 15

Asp Leu Leu Phe Ile Leu Ser Pro Leu Ser Gln Gly Cys Phe Ile Leu  
 20 25 30

Phe Xaa

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Phe Gly Phe Ile Phe Leu Leu Leu Ile Phe Cys Ile Xaa Leu Cys  
 1 5 10 15

Ser Arg Thr Leu Ser Thr Phe Ile Pro Lys Leu Val Gly Phe Leu Tyr  
 20 25 30

Trp Lys Phe Ser Ile Asn Leu Ser Leu Leu Leu Thr Leu Ile Lys Lys  
 35 40 45

Lys Lys Lys Lys Lys Lys Thr Pro Arg Gly Gly Pro Gly Xaa Gln Ser  
 50 55 60

Pro Pro  
 65

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

551

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

5 Met Pro Gly Leu Gly Arg Pro Arg Gln Ala Arg Trp Thr Leu Met Leu  
 1 5 10 15  
 Leu Leu Ser Thr Ala Met Tyr Gly Ala His Ala Pro Leu Leu Ala Leu  
 20 25 30  
 10 Cys His Val Asp Gly Arg Val Pro Phe Arg Pro Ser Ser Ala Val Leu  
 35 40 45  
 Leu Thr Glu Leu Thr Lys Leu Leu Leu Cys Ala Phe Ser Leu Leu Val  
 50 55 60  
 Gly Trp Gln Ala Trp Pro Gln Gly Pro Pro Pro Trp Arg Gln Ala Ala  
 65 70 75 80  
 20 Pro Phe Ala Leu Ser Ala Leu Leu Tyr Gly Ala Asn Asn Asn Leu Val  
 85 90 95  
 Ile Tyr Leu Gln Arg Tyr Met Asp Pro Ser Thr Tyr Gln Val Leu Ser  
 100 105 110  
 25 Asn Leu Lys Ile Gly Ser Thr Ala Val Leu Tyr Cys Leu Cys Leu Arg  
 115 120 125  
 His Arg Leu Ser Val Arg Gln Gly Leu Ala Leu Leu Leu Met Ala  
 130 135 140  
 Ala Gly Ala Cys Tyr Ala Ala Gly Gly Leu Gln Val Pro Gly Asn Thr  
 145 150 155 160  
 35 Leu Pro Ser Pro Pro Pro Ala Ala Ala Ala Ser Pro Met Pro Leu His  
 165 170 175  
 Ile Thr Pro Leu Gly Leu Leu Leu Leu Ile Leu Tyr Cys Leu Ile Ser  
 180 185 190  
 40 Gly Leu Ser Ser Val Tyr Thr Glu Leu Leu Met Lys Arg Gln Xaa Leu  
 195 200 205  
 Pro Leu Ala Leu Gln Asn Leu Phe Leu Tyr Thr Phe Gly Val Leu Leu  
 210 215 220  
 Asn Leu Gly Leu His Ala Gly Gly Gly Ser Gly Pro Gly Leu Leu Glu  
 225 230 235 240  
 50 Gly Phe Ser Gly Trp Ala Ala Leu Val Val Leu Ser Gln Ala Leu Asn  
 245 250 255  
 Gly Leu Leu Met Ser Ala Val Met Lys His Gly Ser Ser Ile Thr Arg  
 260 265 270  
 55 Leu Phe Val Val Ser Cys Ser Leu Val Val Asn Ala Val Leu Ser Ala  
 275 280 285  
 Val Leu Leu Arg Leu Gln Leu Thr Ala Ala Phe Phe Leu Ala Thr Leu  
 290 295 300

552

Leu Ile Gly Leu Ala Met Arg Leu Tyr Tyr Gly Ser Arg  
 305 310 315

5

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

15 Met Gly Glu Gln Pro His Phe Ser Leu Cys Val Leu Leu Ala Ala Val  
 1 5 10 15  
 Arg Glu Asp Xaa Asp Pro Xaa Val Phe Pro Cys Cys Phe Leu Xaa  
 20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

30

Met Ser Phe Ile Ala Leu His Pro Leu Leu Pro Glu Ala Ala Leu Gly  
 1 5 10 15  
 Val Pro Gly Gln Ser Pro His Arg Pro Leu Trp Gln Thr Gln Cys Cys  
 35 20 25 30

35

Val Ala Pro Pro Gln Pro Arg Ala Glu Phe Xaa  
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 255 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

45

50 Met Val Thr Ala Leu Thr Leu Leu Ala Phe Pro Leu Leu Leu His  
 1 5 10 15  
 Ala Glu Arg Ile Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe  
 20 25 30

55

Leu Leu Leu His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly  
 35 40 45

60

Pro Phe Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala  
 50 55 60

553

Thr Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile  
 65 70 75 80  
 5 His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser Cys  
 85 90 95  
 Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala Ser His  
 100 105 110  
 10 Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Trp Pro Phe Leu  
 115 120 125  
 Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro Pro Gly Asn Glu  
 130 135 140  
 15 Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu Glu Pro Leu Met Glu  
 145 150 155 160  
 20 Met Arg Leu Arg Asp Ala Pro Gln His Phe Tyr Ala Ala Leu Leu Gln  
 165 170 175  
 Leu Gly Leu Lys Tyr Leu Phe Ile Leu Gly Ile Gln Ile Leu Ala Cys  
 180 185 190  
 25 Ala Leu Ala Ala Ser Ile Leu Arg Arg His Leu Met Val Trp Lys Val  
 195 200 205  
 Phe Ala Pro Lys Phe Ile Phe Glu Ala Val Gly Phe Ile Val Ser Ser  
 210 215 220  
 30 Val Gly Leu Leu Leu Gly Ile Ala Leu Val Met Arg Val Asp Gly Ala  
 225 230 235 240  
 35 Val Ser Ser Trp Phe Arg Gln Leu Phe Leu Ala Gln Gln Arg Xaa  
 245 250 255

40 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Xaa Gly Pro Trp Gly Glu Glu Ala Leu Ile Arg Leu Pro Thr Pro  
 1 5 10 15  
 50 Ser Gly Leu Xaa  
 20

55

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

60

554

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

5 Met Ala Thr Leu Glu Xaa Asn Gln Arg Glu Val Asp Arg Glu Ile Arg  
 1 5 10 15  
 Ser Leu Leu Leu Trp Phe Leu Leu Cys Glu Ile Val Ser Gly Trp Leu  
 20 25 30  
 10 Cys Pro Glu Gly Pro Trp Phe Ser Gln Gly Cys Gln Ile Tyr Lys Asn  
 35 40 45  
 Leu Ser Ser Ser Ser Ser Tyr Asn Leu Ser Phe Leu Leu Ser Leu Xaa  
 50 55 60

20

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

30 Met Ile His Ser Gly Cys Thr Ser Gln Cys Leu Glu Gly Phe Phe Leu  
 1 5 10 15  
 Ile Phe Leu Leu Asp Phe Asn Pro Val Leu Ala Leu Asp Leu Ile Gly  
 20 25 30  
 35 Ile Met Arg Lys Ala Ser His Xaa  
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

50 Met Val Phe Ser Ala Arg Val Ser Leu Tyr Thr Arg Phe Lys Val Ile  
 1 5 10 15  
 Leu Leu Ser Leu Leu Ile Met Ile Leu His Val Cys Trp Val Trp Val  
 20 25 30  
 55 Ile Leu Xaa  
 35

60

(2) INFORMATION FOR SEQ ID NO: 375:



555

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Gly Leu Leu Tyr Ile Met Tyr Cys Asn Ile Xaa  
1 5 10

10

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

20 Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro  
1 5 10 15

Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser  
20 25 30

25

Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys  
35 40 45

30

Ser Gly Gly Arg Asp His Thr Gly Gly Asn Lys Asp Arg Gly Ile Xaa  
50 55 60

35

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

45 Met Arg Lys Gln Arg Leu Val Pro Met Tyr Leu Gly Leu Ile Tyr Ile  
1 5 10 15

Leu Leu Xaa

50

## (2) INFORMATION FOR SEQ ID NO: 378:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

60

556

Met Arg Gln His Xaa

1 5

5

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

10

15

Leu Leu Leu Pro Val Leu Ala Ser Ser Val Pro Ser His Ser Ala Thr  
1 5 10 15

Xaa

20

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

25

30

Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn Ser Phe Leu His Gln  
1 5 10 15Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser Leu Val Ala Ile Leu  
20 25 30

35

Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys Val Gln Leu Asp Ala  
35 40 45

40

Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile Val Leu Ile Asn Ser  
50 55 60Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly Leu Ala Gly Leu Leu  
65 70 75 80

45

Pro Ala Ser Xaa

50

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

55

60

Met Lys Leu Ser Leu Phe Leu Ile Leu Ser Asp Val Phe Tyr Leu Gly  
1 5 10 15

Ser Pro Xaa Thr Xaa  
20

5

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

10

Met Gly Thr Arg Arg Lys Gly Val Ala Trp Leu Ser Leu Ala Pro Leu  
1 5 10 15

15

Ile Thr Gly Leu Ala Pro Ala His Ile Thr Ala Val Xaa  
20 25

20

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

25

Met Lys Asp Leu Leu Gln Arg Asn Pro Trp Lys Asn Ser Leu Leu Leu  
1 5 10 15

30

Leu Gln Val Cys Gln Ala Phe Leu Val Cys Ser Leu Thr Gln Leu Ala  
20 25 30

35

Val Xaa

40

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

45

Met Ser Glu Ser His Lys Ile Trp Trp Cys Tyr Arg His Leu Ala Phe  
1 5 10 15

50

Pro Leu Leu Thr Leu Ile Leu Tyr Pro Ala Thr Leu Gly Arg Ser Val  
20 25 30

55

Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Xaa  
35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 385:

558

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Leu Asn Arg Ile Met Val Ala Ser Phe Gly Ala Val Leu Val Gln  
 1 5 10 15  
 Val Cys Arg Gly Xaa Gly Gln Gly Xaa  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 386:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Gln Leu Leu Leu Leu Gly Leu Ile Arg Ser Gln Pro Ser Pro Pro  
 1 5 10 15  
 Pro Ser Leu Cys Leu Met Leu Cys Pro Cys Leu Pro Cys Leu Arg Tyr  
 20 25 30  
 Ser Pro Phe Val Pro Gln His Pro Cys Pro Leu Pro Leu Asp Leu Cys  
 35 40 45  
 Leu Ala Gly Cys Ser Ser Leu Ser Val Gln Asp Lys Cys Ser Trp Pro  
 50 55 60  
 Tyr Pro Ile Xaa  
 65

## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Lys Glu Phe Phe Val Phe Leu Phe Val Cys Leu Phe Trp Leu Leu Ser  
 1 5 10 15  
 Asn Thr Pro Leu Thr Phe Ile Ser Ile Ile Leu Gln Arg Lys Glu Thr  
 20 25 30  
 Asn Xaa

## (2) INFORMATION FOR SEQ ID NO: 388:

559

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Ser Phe Leu Met Val Leu Val Ile Leu Ala Ala Ser Pro Xaa  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

1 5 10

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser Val  
 1 5 10 15

Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly Ala Ala  
 20 25 30

His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr Gly Pro Pro  
 35 40 45

Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu Thr Ala Asp Ser  
 50 55 60

Asp Val Asp Xaa Phe Leu Asp Xaa Phe Leu Ser Ala Gly Val Lys Gln  
 65 70 75 80

Ser Asp Xaa Pro Arg Lys Glu Thr Glu Gln Pro Pro Ala Pro Gly Ser  
 85 90 95

Met Glu Glu Ser Val Arg Xaa Tyr Asp Trp Ser Pro Arg Xaa Ala Arg  
 100 105 110

Arg Thr Gln Thr Arg Ala Gly Ser Xaa Arg Xaa Gly Gly Xaa Cys Cys  
 115 120 125

Gly Ala Ser Ala Pro Xaa Pro Ala Trp Pro Ser Pro Pro Arg Ser Ala  
 130 135 140

His Ser Thr Thr Ser Pro Thr Arg Ser Xaa  
145 150

5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids.

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Val Leu Leu Gly Leu Leu Ser Xaa  
1 5

15

(2) INFORMATION FOR SEQ ID NO: 392:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Cys Ile His Val Phe Met Xaa Val Leu Trp Val Leu Phe Leu Leu  
1 5 10 15

30

Asn Pro Leu Cys Thr Gly Leu Trp Pro Leu Xaa Asn Cys Phe Ser Val  
20 25 30

Leu Arg His Ala Asp Trp Val Leu Gly Ala Asp Tyr Lys Gly Glu Glu  
35 40 45

35

Leu Asn Arg His Gln Gly Pro Met Lys Pro Lys Asp Xaa  
50 55 60

40

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser  
1 5 10 15

50

His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser  
20 25 30

55

Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp  
35 40 45

Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu  
50 55 60

60

561

Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu  
 65 70 75 80  
 5 Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg  
 85 90 95  
 Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr  
 100 105 110  
 10 Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu  
 115 120 125  
 Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg  
 130 135 140  
 15 Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn  
 145 150 155 160  
 Val Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys  
 165 170 175  
 Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe  
 180 185 190  
 25 Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu  
 195 200 205  
 Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu  
 210 215 220  
 30 Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser  
 225 230 235 240  
 Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln  
 245 250 255  
 Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys  
 260 265 270  
 40 Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala  
 275 280 285  
 Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu  
 290 295 300  
 45 Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu  
 305 310 315 320  
 Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu Glu Ala Glu  
 325 330 335  
 50 Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr Arg Gln Val  
 340 345 350  
 55 His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu Ile Thr Ala  
 355 360 365  
 His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys Val Leu Gln  
 370 375 380  
 60

562

Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp  
385 390 395 400

Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val  
405 410 415

Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln  
420 425 430

Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg Xaa  
435 440 445

15 (2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Val Ile Ser Tyr Val Thr Phe Thr Pro Val Ser Ala Asp Cys Phe  
1 5 10 15

Phe Asn Val Leu Val Cys Phe Xaa  
20

30 (2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Glu Leu Leu Phe Leu Leu Ile Ile Ile Leu Gly Glu Ser Leu Ser Asp  
1 5 10 15

Val Ile Leu Leu Ile Cys Phe Xaa  
20

45 (2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Phe Tyr Trp Gly Gly Leu Ser Phe Tyr Phe Leu Leu Ser Ser Gly  
1 5 10 15

Val Gly Phe Tyr Cys Phe Leu Phe Gly Phe Gly Met Glu Ile Trp Ile  
20 25 30



Ala Ala Xaa  
35

5

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Gly Arg Xaa

15

1

(2) INFORMATION FOR SEQ ID NO: 398:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Lys Leu Ser Leu Leu Ile Leu Thr Leu Met Gln Arg Tyr Phe Arg  
1 5 10 15

30

Thr Ile Thr Asn Ser Leu Cys Lys Xaa  
20 25

35

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Pro Ala Val Ser Gly Pro Gly Pro Leu Phe Cys Leu Leu Leu Leu  
1 5 10 15

45

Leu Leu Asp Pro His Ser Pro Glu Thr Gly Cys Pro Pro Leu Arg Arg  
20 25 30

50

Phe Glu Tyr Lys Leu Ser Phe Lys Gly Pro Arg Leu Ala Leu Pro Gly  
35 40 45

Ala Gly Ile Pro Phe Trp Ser His His Gly Gly Glu Gly Gln Gly Trp  
50 55 60

55

Gly Pro Leu Cys Pro Gly Ser Leu Lys Val Leu Glu Gly Leu Xaa  
65 70 75

60

(2) INFORMATION FOR SEQ ID NO: 400:

564

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Lys Val Phe Leu Ser Met Pro Phe Leu Val Leu Phe Gln Ser Leu  
 1 5 10 15  
 Ile Gln Glu Asp Xaa  
 20

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Ala Ala Leu Thr Ser His Leu Gln Asn Gln Ser Asn Asn Ser Asn  
 1 5 10 15  
 Trp Asn Leu Arg Thr Arg Ser Lys Cys Lys Lys Asp Val Phe Met Pro  
 20 25 30  
 Pro Ser Ser Ser Ser Glu Leu Gln Glu Ser Arg Gly Leu Ser Asn Phe  
 35 40 45  
 Thr Ser Thr His Leu Leu Leu Lys Glu Asp Glu Gly Val Asp Asp Val  
 50 55 60  
 Asn Phe Arg Lys Val Arg Lys Pro Lys Gly Lys Val Thr Ile Leu Lys  
 65 70 75 80  
 Gly Ile Pro Ile Lys Lys Thr Lys Lys Gly Cys Arg Lys Ser Cys Ser  
 85 90 95  
 Gly Phe Val Xaa Ser Asp Ser Lys Arg Glu Ser Val Cys Asn Lys Ala  
 100 105 110  
 Asp Ala Glu Ser Glu Pro Val Ala Gln Lys Ser Gln Leu Asp Arg Thr  
 115 120 125  
 Val Cys Ile Ser Asp Ala Gly Ala Cys Gly Glu Thr Leu Ser Val Thr  
 130 135 140  
 Ser Glu Glu Asn Ser Leu Val Lys Lys Lys Glu Arg Ser Leu Ser Ser  
 145 150 155 160  
 Gly Ser Asn Phe Cys Ser Glu Gln Lys Thr Ser Gly Ile Ile Asn Lys  
 165 170 175  
 Phe Cys Ser Ala Lys Asp Ser Glu His Asn Glu Lys Tyr Glu Asp Thr  
 180 185 190  
 Phe Leu Glu Ser Glu Glu Ile Gly Thr Lys Val Glu Val Val Glu Arg

195

205

5

Arg Asn Thr Asp Arg Lys Lys Glu Asn Lys Pro Val Phe Phe Gln Gln  
245 250 255

15

20

(D) TOPOLOGY: linear

25

30

35

40.

45

50

Arg Leu Asn Trp Ile Gln Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser  
145                      150                      155                      160

60

566

Leu Leu Phe Arg Asn Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys  
 195 200 205  
 5 Glu Trp Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe  
 210 215 220  
 Ser His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys  
 225 230 235 240  
 10 Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys Glu  
 245 250 255  
 Gly Asn Gln Leu Thr Glu Xaa Ile Phe Ile Gln Asn Ser Lys Leu Tyr  
 260 265 270  
 15 Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu Gln Arg Ser  
 275 280 285  
 Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr Gly His Ser Ala  
 290 295 300  
 Phe Ser Val Ala Leu Ile Phe Val Thr Ala Phe Gln Gly Leu Ser Val  
 305 310 315 320  
 25 Ala Phe Ile Leu Lys Phe Leu Asp Asn Met Phe His Val Leu Met Ala  
 325 330 335  
 Gln Val Thr Thr Val Ile Ile Thr Thr Val Ser Val Leu Val Phe Asp  
 340 345 350  
 30 Phe Arg Pro Ser Leu Glu Phe Phe Leu Glu Ala Pro Ser Val Leu Leu  
 355 360 365  
 Ser Ile Phe Ile Tyr Asn Ala Ser Lys Pro Gln Val Pro Glu Tyr Ala  
 370 375 380  
 Pro Arg Gln Glu Arg Ile Arg Asp Leu Ser Gly Asn Leu Trp Glu Arg  
 385 390 395 400  
 40 Ser Ser Gly Asp Gly Glu Glu Leu Glu Arg Leu Thr Lys Pro Lys Ser  
 405 410 415  
 Asp Glu Ser Asp Glu Asp Thr Phe  
 420  
 45

(2) INFORMATION FOR SEQ ID NO: 403:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:  
 Met Trp Gly Gln Gly Ser Gln Lys Ser His Phe Ser Asp Leu Val Phe  
 1 5 10 15  
 Gly Val Arg Glu Leu Cys Ala Gln Pro Ser Asp Pro Gly Ser Pro His  
 20 25 30  
 60

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 404:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

15

Met Val Gln His Ile Gln Pro Ala Ala Leu Ser Leu Leu Ala Gln Trp  
 1 5 10 15

Ser Thr Leu Val Gln Glu Leu Glu Ala Ala Leu Gln Leu Ala Phe Tyr  
 20 25 30

20

Pro Asp Ala Val Glu Glu Trp Leu Glu Glu Asn Val His Pro Ser Leu  
 35 40 45

25

Gln Arg Leu Gln Xaa Leu Leu Gln Asp Leu Ser Glu Val Ser Ala Pro  
 50 55 60

Pro Leu Pro Pro Thr Ser Pro Gly Arg Asp Val Ala Gln Asp Pro Xaa  
 65 70 75 80

30

35

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

40

Met Leu Asn Gln Gly Tyr Ile Arg Lys Ile Ile Leu Ile Ile Ile Leu  
 1 5 10 15

45

Gly Ser Phe Ser Ser Pro Lys Lys Ala Ile Leu Met Gly Phe Gln Asn  
 20 25 30

50

Gln Lys Lys Ala Leu Asn Glu Glu Gln Thr Thr Gly Val Pro Met Ser  
 35 40 45

Ile Ser Gly Lys Leu Arg Pro Ser Arg Ser Leu Asp Phe Val Gln Pro  
 50 55 60

55

Pro Arg Phe Gln Ser Gln Gln Pro Ser Ala Val Val Asp Arg Arg Gly  
 65 70 75 80

Phe Xaa Xaa Lys Ala Ala Arg Gly Gln Glu Phe Ser Glu Ser Xaa  
 85 90 95

60

## (2) INFORMATION FOR SEQ ID NO: 406:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:  
 10 Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln  
 1 Ala 5 10 15  
 15 Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Leu Val  
 20 25 30  
 Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro  
 35 40 45  
 20 Thr Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr  
 50 55 60  
 His Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu  
 65 70 75 80  
 25 Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro  
 85 90 95  
 His Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu  
 100 105 110  
 Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro  
 115 120 125  
 35 Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp  
 130 135 140  
 Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr  
 145 150 155 160  
 40 Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser  
 165 170 175  
 Phe Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe  
 180 185 190  
 45 Phe His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr  
 195 200 205  
 50 Tyr His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp  
 210 215 220  
 Arg Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln  
 225 230 235 240  
 55 Asn Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile  
 245 250 255  
 60 Phe

570

	260	265	270
	Val Ser Leu Lys Glu Ser Asp Arg His Thr Leu Leu His Phe Leu Glu		
	275	280	285
5	Asp Glu Lys Tyr Glu Glu Val Met Ala Val Leu Gly Ser Phe Pro Tyr		
	290	295	300
10	Val Thr Met Asp Ile Lys Ser Gln Val Leu Asp Asp Glu Asp Ser Asn		
	305	310	315 320
	Asn Ile Thr Val Gly Ser Leu Val Thr Val Leu Val Lys Leu Thr Arg		
	325	330	335
15	Gln Thr Met Ala Glu Val Phe Glu Lys Glu Gln Ser Ile Cys Ala Ala		
	340	345	350
	Glu Glu Gln Pro Ala Glu Asp Gly Gln Gly Glu Thr Asn Lys Asn Arg		
	355	360	365
20	Thr Lys Gly Gly Trp Gln Gln Lys Ser Lys Gly Pro Lys Lys Thr Ala		
	370	375	380
25	Lys Ser Lys Lys Lys Lys Pro Leu Lys Lys Lys Pro Thr Pro Val Leu		
	385	390	395 400
	Leu Pro Gln Ser Lys Gln Gln Lys Gln Lys Gln Ala Asn Gly Val Val		
	405	410	415
30	Gly Asn Glu Ala Ala Val Lys Glu Asp Glu Glu Glu Val Ser Asp Lys		
	420	425	430
	Gly Ser Asp Ser Glu Glu Glu Glu Thr Asn Arg Asp Ser Gln Ser Glu		
	435	440	445
35	Lys Asp Asp Gly Ser Asp Arg Asp Ser Asp Arg Glu Gln Asp Glu Lys		
	450	455	460
40	Gln Asn Lys Asp Asp Glu Ala Glu Trp Gln Glu Leu Gln Gln Ser Ile		
	465	470	475 480
	Gln Arg Lys Glu Arg Ala Leu Leu Glu Thr Lys Ser Lys Ile Thr His		
	485	490	495
45	Pro Val Tyr Ser Leu Tyr Phe Pro Glu Glu Lys Gln Glu Trp Trp Trp		
	500	505	510
	Leu Tyr Ile Ala Asp Arg Lys Glu Gln Thr Leu Ile Ser Met Pro Tyr		
	515	520	525
50	His Val Cys Thr Leu Lys Asp Thr Glu Glu Val Glu Leu Lys Phe Pro		
	530	535	540
	Ala Pro Gly Lys Pro Gly Asn Tyr Gln Tyr Thr Val Phe Leu Arg Ser		
	545	550	555 560
55	Asp Ser Tyr Met Gly Leu Asp Gln Ile Lys Pro Leu Glu Val Xaa Lys		
	565	570	575
60	Phe Met Arg Leu Lys Pro Val Pro Glu Asn His Pro Gln Trp Asp Thr		

## (2) INFORMATION FOR SEQ ID NO: 407:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 amino acids

(B) TYPE: amino-acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

5 Met Phe Met Arg Ile Ala Lys Ala Tyr Ala Ala Leu Thr Asp Glu Glu  
 1 5 10 15  
 15 Ser Arg Lys Asn Trp Glu Glu Phe Gly Asn Pro Asp Gly Pro Gln Ala  
 20 25 30  
 Thr Ser Phe Gly Ile Ala Leu Pro Ala Trp Ile Val Asp Gln Lys Asn  
 35 40 45  
 20 Ser Ile Leu Val Leu Leu Val Tyr Gly Leu Ala Phe Met Val Ile Leu  
 50 55 60  
 Pro Val Val Val Gly Ser Trp Trp Tyr Arg Ser Ile Arg Tyr Ser Gly  
 25 65 70 75 80  
 Asp Gln Ile Leu Ile Arg Thr Thr Gln Ile Tyr Thr Tyr Phe Val Tyr  
 85 90 95  
 30 Lys Thr Arg Asn Met Asp Met Lys Arg Leu Ile Met Val Leu Xaa Gly  
 100 105 110  
 Ala Ser Glu Phe Asp Pro Gln Tyr Asn Lys Asp Ala Thr Ser Arg Pro  
 115 120 125  
 35 Thr Asp Asn Ile Leu Ile Pro Gln Leu Ile Arg Glu Ile Gly Ser Ile  
 130 135 140  
 Asn Leu Lys Lys Asn Glu Pro Pro Leu Thr Cys Pro Tyr Ser Leu Lys  
 40 145 150 155 160  
 Ala Arg Val Leu Leu Leu Ser His Leu Ala Arg Met Lys Ile Pro Glu  
 165 170 175  
 45 Thr Leu Glu Glu Asp Gln Gln Phe Met Leu Lys Lys Cys Pro Ala Leu  
 180 185 190  
 Leu Gln Glu Met Val Asn Val Ile Cys Gln Leu Ile Val Met Ala Arg  
 195 200 205  
 50 Asn Arg Glu Glu Arg Glu Phe Arg Ala Pro Thr Leu Ala Ser Leu Glu  
 210 215 220  
 Asn Cys Met Lys Leu Ser Gln Met Ala Val Gln Gly Leu Gln Gln Phe  
 225 230 235 240  
 Lys Ser Pro Leu Leu Gln Leu Pro His Ile Glu Glu Asp Asn Leu Arg  
 245 250 255  
 60 Arg Val Ser Asn His Lys Lys Tyr Lys Ile Lys Thr Ile Gln Asp Leu



571

580

585

590

Ala Ile Glu Gly Asp Glu Asp Gln Glu Asp Ser Glu Gly Phe Glu Asp  
595 600 605

Ser Phe Glu Gly Gly Arg Gly Arg Glu Glu Gly Arg Trp Trp Thr  
610 615 620

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Lys Ala Ser Gln Cys Cys Cys Cys Leu Ser His Leu Leu Ala Ser  
1 5 10 15

Val Leu Leu Leu Leu Leu Leu Pro Glu Leu Ser Gly Xaa Leu Xaa Val  
20 25 30

Leu Leu Gln Ala Ala Glu Ala Ala Pro Gly Leu Gly Pro Pro Asp Pro  
35 40 45

Arg Pro Arg Thr Leu Pro Pro Leu Pro Pro Gly Pro Thr Pro Ala Gln  
50 55 60

Gln Pro Gly Arg Gly Leu Ala Glu Ala Ala Gly Pro Arg Gly Ser Glu  
65 70 75 80

Gly Gly Asn Gly Ser Asn Pro Val Ala Gly Leu Glu Thr Asp Asp His  
85 90 95

Gly Gly Lys Ala Gly Glu Gly Ser Val Gly Gly Gly Leu Ala Val Ser  
100 105 110

Pro Asn Pro Gly Asp Lys Pro Met Thr Gln Arg Ala Leu Thr Val Leu  
115 120 125

Met Val Val Ser Gly Ala Val Leu Val Tyr Phe Val Val Arg Thr Val  
130 135 140

Arg Met Arg Arg Arg Asn Arg Lys Thr Arg Arg Tyr Gly Val Leu Asp  
145 150 155 160

Thr Asn Ile Glu Asn Met Glu Leu Thr Pro Leu Glu Gln Asp Asp Glu  
165 170 175

Asp Asp Asp Asn Thr Leu Phe Asp Ala Asn His Pro Arg Arg  
180 185 190

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

572

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

5 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile  
 1 5 10 15

Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser  
 20 25 30

10 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp  
 35 40 45

15 Ala Val Tyr Thr Gln Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro  
 50 55 60

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly  
 65 70 75 80

20 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Lys Ser Thr Lys  
 85 90 95

Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser  
 100 105 110

25 Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly  
 115 120 125

30 Phe His Glu Asp Asp Pro Phe Phe Tyr Asp Glu His Thr Leu Arg Lys  
 130 135 140

Arg Gly Leu Leu Val Ala Ala Val Leu Phe Ile Thr Gly Ile Ile Ile  
 145 150 155 160

35 Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Arg Leu Cys Arg Asn His  
 165 170 175

Cys Arg Xaa

40

(2) INFORMATION FOR SEQ ID NO: 410:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Phe Lys Cys Leu Gln Thr Thr Phe Leu Phe Ile Xaa Xaa  
 1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

60

(B) TYPE: amino acid

573

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

5 Met Leu Ala Gly Lys Leu Ile Pro Val His Gln Val Arg Gly Leu Lys  
 1 5 10 15  
 Glu Lys Ile Val Arg Ser Phe Glu Val Ser Pro Asp Gly Ser Phe Leu  
 20 25 30  
 10 Leu Ile Asn Gly Ile Ala Gly Tyr Leu His Leu Leu Ala Met Lys Thr  
 35 40 45  
 Lys Glu Leu Ile Gly Ser Met Lys Ile Asn Gly Arg Val Ala Ala Ser  
 50 55 60  
 15 Thr Phe Ser Ser Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly Asp Gly  
 65 70 75 80  
 20 Glu Val Tyr Val Trp Asp Val Asn Ser Arg Lys Cys Leu Asn Arg Phe  
 85 90 95  
 Val Asp Glu Gly Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser Arg Asn  
 100 105 110  
 25 Gly Gln Tyr Val Ala Cys Gly Ser Asn Cys Gly Val Val Asn Ile Tyr  
 115 120 125  
 Asn Gln Asp Ser Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile Lys Ala  
 130 135 140  
 30 Ile Met Asn Leu Val Thr Gly Val Thr Ser Leu Thr Phe Asn Pro Thr  
 145 150 155 160  
 35 Thr Glu Ile Leu Ala Ile Ala Ser Glu Lys Met Lys Glu Ala Val Arg  
 165 170 175  
 Leu Val His Leu Pro Ser Cys Thr Val Phe Ser Asn Phe Pro Val Ile  
 180 185 190  
 40 Lys Asn Lys Asn Ile Ser His Val His Thr Met Asp Phe Ser Pro Arg  
 195 200 205  
 Ser Gly Tyr Phe Ala Leu Gly Asn Glu Lys Gly Lys Ala Leu Met Tyr  
 210 215 220  
 45 Arg Leu His His Tyr Ser Asp Phe  
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

60

Ile Leu Leu Cys Ser Trp Pro Thr Gly Leu Val Gly Gly Arg Asp Pro  
 1 5 10 15

574

Gly Ser Ser Arg Gly Ser Ser Ala Ser Leu Thr Pro Ser Pro Gly Arg  
 20 25 30

5 Gln Pro Cys Ser Arg Arg Arg Gly Tyr Ser Val Gly Arg Arg Ser Ser  
 35 40 45

Pro Pro Asp Gly Ser Xaa  
 50

10

(2) INFORMATION FOR SEQ ID NO: 413:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

20

Met Ser Leu Gln Ser Asn Ala Trp Ser Lys Xaa Leu Phe Ile Val Phe  
 1 5 10 15

25

Leu Phe Leu Arg Val Leu Phe Lys Thr Gly Val Ser Ser Glu Glu Ser  
 20 25 30

Xaa

30

(2) INFORMATION FOR SEQ ID NO: 414:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

40

Met Ala Val Val Leu Leu Ala Asn Leu Ala Gln Gly Asp Ser Leu Ala  
 1 5 10 15

45

Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile Gly Asn Leu Leu Gly  
 20 25 30

Phe Leu Glu Asp Ser Leu Ala Ala Thr Gln Phe Gln Gln Ser Gln Ala  
 35 40 45

50

Ser Leu Leu His Met Gln Asn Pro Pro Phe Glu Pro Xaa Ser Val Asp  
 50 55 60

Met Met Arg Arg Ala Ala Arg Ala Leu Leu Ala Leu Ala Lys Val Asp  
 65 70 75 80

55

Glu Asn His Ser Glu Phe Thr Leu Tyr Glu Ser Arg Leu Leu Asp Ile  
 85 90 95

Ser Val Ser Pro Leu Met Asn Ser Xaa Val Ser Gln Val Ile Cys Asp  
 100 105 110

60

575

Val Leu Phe Leu Xaa Trp Pro Val Met Thr Ala Val Gly His Leu Pro  
115 120 125

5 Pro Pro Cys Val Cys Ala Cys Val Glu Asn Leu Glu Thr Asp Cys Cys  
130 135 140

Pro Leu Phe Met Gln Asn His Leu Arg Ile Gln Phe Thr Leu Cys Cys  
145 150 155 160

10 Pro Ala Ser Pro Leu Gly Lys Ser Leu Ser Cys Phe Ser Leu Leu Leu  
165 170 175

Pro Pro Pro Leu Pro Pro Ser Pro His Ala Phe Leu Phe Leu Val Leu  
180 185 190

15 Thr Leu Leu Pro Ser Gly Pro Tyr Pro Thr Leu Phe Glu Lys Thr Lys  
195 200 205

20 Leu Cys Leu His Arg Arg Leu Phe Leu Phe Xaa  
210 215

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Leu Pro Asp Glu Ser Phe Gly Leu Leu Leu Ser Ile Pro Ser Leu  
1 5 10 15

35 Thr Pro Ser Ala Ala Ala Pro Ser Phe Cys Val His Leu Met Gln Ala  
20 25 30

Ser Arg Ser Ser Lys Arg Ala Ser His Val Pro Val His Leu Leu Trp  
35 40 45

40 Gly Asp Xaa  
50

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Arg Pro Gly Ser Phe Ser Phe Ile Ala Phe Leu Ala Thr Glu Val  
1 5 10 15

Ser Ser Cys Phe Pro Gly Arg Pro Asp Cys Xaa Thr Gly Met Trp Leu  
20 25 30

60 Leu Gln Leu Gln Lys Lys Gln Arg Thr Leu Leu Ala Met Ala Pro Arg

576

35

40

45

Arg Xaa  
50

5

(2) INFORMATION FOR SEQ ID NO: 417:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Asp Arg Pro Cys Pro Ser Ser Leu Trp Lys Val Phe Pro Leu Leu Leu  
1 5 10 15

20

Leu Leu Met Arg Leu Phe Pro Leu Pro Val Pro Gly Asn Gln Arg Ala  
20 25 30

Xaa Leu Pro His Pro Phe Xaa Ala Pro Arg Leu Pro Cys Leu Leu Cys  
35 40 45

25

Leu Cys Thr Gln Gln Phe Xaa Val Cys Ser His Tyr Leu Pro Ala Gly  
50 55 60

Tyr Arg Val Asn Ser Xaa  
65 70

30

(2) INFORMATION FOR SEQ ID NO: 418:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met His Glu Lys Ala Trp Asn Leu Ile Leu Leu Trp Trp Leu Ser Leu  
1 5 10 15

45

Asp Leu Leu Gly Val Ala Lys Thr Ala Met Trp Ala Gln Trp Cys Gly  
20 25 30

Leu Asn Asp His Lys Gly Lys Xaa  
35 40

50

(2) INFORMATION FOR SEQ ID NO: 419:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

60

Met Ala Phe Val Leu Leu Xaa Cys Phe Val Xaa Leu Gln Ser Ser Xaa

577

1                    5                    10                    15  
 Gly Arg Ala Val Gln Xaa  
                     20

5

(2) INFORMATION FOR SEQ ID NO: 420:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

15

Met Phe Ser Leu Leu Trp Leu Val Cys Val Pro Ser Asn Ser Ser Val  
   1                    5                    10                    15

20

Ala Asn Val Thr Ala Ser Arg Gly Gly Val Phe Lys Arg Ser Leu Gly  
                     20                    25                    30

His Glu Gly Phe Ser Xaa  
                     35

25

(2) INFORMATION FOR SEQ ID NO: 421:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

35

Lys Trp Leu Leu Phe Ile Phe Leu Leu Cys Leu Gln Leu Val Asn Ala  
   1                    5                    10                    15

40

Leu Leu Ser Leu Phe Gln Glu Arg Phe Val His Cys Pro Ala Arg Phe  
                     20                    25                    30

Val Ser Xaa  
                     35

45

(2) INFORMATION FOR SEQ ID NO: 422:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

55

Met Leu Leu Phe Leu Ser Ile Thr Asn Ser Leu Ser Phe Ile Ser Val  
   1                    5                    10                    15

Asp Lys Pro Phe Gly Gln Ser Glu Arg Val Cys Pro Val Ile Ser Xaa  
                     20                    25                    30

60

## 5 (2) INFORMATION FOR SEQ ID NO: 423:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

15 Met Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys  
 1 5 10 15  
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly  
 20 25 30  
 20 Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn Tyr Ile  
 35 40 45  
 His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val Leu  
 50 55 60  
 25 Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu Leu Cys Glu Ala  
 65 70 75 80  
 Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val Ala  
 85 90 95  
 30 Gly Ile Gly Leu Val Val Leu Phe Phe Ser Trp Met Leu Ser Ile Phe  
 100 105 110  
 Arg Ser Lys Tyr His Gly Tyr Pro Tyr Ser Phe Leu Met Ser Xaa  
 115 120 125  
 35

## 40 (2) INFORMATION FOR SEQ ID NO: 424:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

50 Met Thr Trp His Ser Arg Glu Ser Phe Xaa Leu Leu Arg Val Val Ala  
 1 5 10 15  
 Pro Ser Gln Ala Pro Gly Met Gln Val Ser Pro Ser Gln Arg Ala Trp  
 20 25 30  
 Arg Arg Pro Leu His Arg Cys His Val Ala Ala Pro Arg Pro His His  
 35 40 45  
 55 Phe Ala Phe Phe Arg Asn Pro Phe Ser Trp Ser Phe Ile Lys Leu Leu  
 50 55 60  
 Tyr Arg Tyr Leu Xaa  
 60 65



## (2) INFORMATION FOR SEQ ID NO: 425:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val  
 1 5 10 15

Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp  
 20 25 30

Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Thr  
 35 40 45

Trp Pro Thr Thr Arg Ser Leu Gly Arg Gln Asp Glu His Gln Asp Arg  
 50 55 60

Val His Ile Leu Gly Gly Phe Pro Gln Leu His Gly His Ser Pro Tyr  
 65 70 75 80

Gly Leu Pro Gly Arg Gly Glu Arg Tyr Val Gly Xaa  
 85 90

## (2) INFORMATION FOR SEQ ID NO: 426:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser  
 1 5 10 15

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln  
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile  
 65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln  
 85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly  
 100 105 110

580

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro  
 115 120 125  
 5 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln  
 130 135 140  
 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu  
 145 150 155 160  
 10 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr  
 165 170 175  
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys  
 180 185 190  
 15 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His  
 195 200 205  
 20 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys  
 210 215 220  
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn  
 225 230 235 240  
 25 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys  
 245 250 255  
 Phe Tyr Pro Gly Lys Cys Ile Xaa Pro Pro Gly Leu Glu Gly Glu Gln  
 260 265 270  
 30 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys  
 275 280 285  
 35 Ile Gly Lys Ser Lys Cys Lys Xaa Ser Lys Gly Tyr Gln Gly Asp Leu  
 290 295 300  
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys  
 305 310 315 320  
 40 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His  
 325 330 335  
 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala  
 340 345 350  
 45 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365  
 50 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp Xaa  
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 427:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Thr Ser Asn Leu Leu Leu Leu Thr Leu Leu Leu Lys Asp Thr Leu  
 1 5 10 15

5 Xaa Leu Ala Lys Xaa Asn Xaa Xaa  
 20

10 (2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Arg His His Thr Gln Leu Asn Phe Ile Phe Leu Val Glu Met Val  
 1 5 10 15

20 Phe Leu His Val Gly Gln Ala Gly Leu Lys Leu Pro Thr Ser Gly Asp  
 20 25 30

25 Xaa Ala Cys Phe Gly Leu Pro Lys Val Leu Gly Leu Gln Ala Xaa  
 35 40 45

30 (2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Cys Ser Asp Xaa  
 1 5

40

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

50 Leu Leu Ser Ile Leu Leu Cys Leu Leu Ala Ser Gly Leu Val Val Phe  
 1 5 10 15

Phe Leu Phe Pro His Ser Val Leu Val Asp Asp Asp Gly Ile Lys Val  
 20 25 30

55 Val Lys Val Thr Phe Asn Lys Gln Asp Ser Leu Val Ile Leu Thr Ile  
 35 40 45

60 Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala Val  
 50 55 60

582

Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Asn Phe  
 65 70 75 80  
 5 Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe  
 85 90 95  
 Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val Ile Phe Met Arg  
 100 105 110  
 10 Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu  
 115 120 125  
 Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser Thr Ala Ile Xaa  
 15 130 135 140

20

(2) INFORMATION FOR SEQ ID NO: 431:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

30 Met Phe Phe Phe Leu Tyr Val Tyr Ser Val Leu Cys Gly Leu Leu Val  
 1 5 10 15  
 Tyr Pro Ser Leu Pro Ser His Ser Val Ser Leu Val Thr Ser Leu Val  
 20 25 30  
 35 Ala Ser Ala Leu Xaa  
 35

40

(2) INFORMATION FOR SEQ ID NO: 432:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

50 Met Ala Ser Ile Asn Ala Val Tyr Ile His Val Phe Leu Gly Val Cys  
 1 5 10 15  
 Val Gln Ala Thr Ala Ala Cys Pro Trp Cys Ser Gln Cys Arg Xaa Gly  
 20 25 30  
 55 Ser Val Pro Ser Xaa  
 35

60 (2) INFORMATION FOR SEQ ID NO: 433:

583

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

5 Met Met Ala Ala Met Val Leu Thr Ser Leu Ser Cys Ser Pro Val Val  
 1 5 10 15  
 10 Gln Ser Pro Pro Gly Thr Glu Ala Asn Phe Ser Ala Ser Arg Ala Ala  
 20 25 30  
 15 Cys Asp Pro Trp Lys Glu Ser Gly Asp Ile Ser Asp Ser Gly Xaa Ser  
 35 40 45  
 Thr Thr Ser Gly His Trp Ser Gly Ser Ser Gly Val Ser Thr Pro Ser  
 50 55 60  
 20 Pro Pro His Pro Gln Ala Ser Pro Lys Tyr Leu Gly Asp Ala Phe Gly  
 65 70 75 80  
 Ser Pro Gln Thr Asp His Gly Phe Glu Thr Asp Pro Asp Pro Phe Leu  
 85 90 95  
 25 Leu Asp Glu Pro Ala Pro Arg Lys Arg Lys Asn Ser Val Lys Val Met  
 100 105 110  
 30 Tyr Lys Cys Leu Trp Pro Asn Cys Gly Lys Val Leu Arg Ser Ile Val  
 115 120 125  
 Gly Ile Lys Arg His Val Lys Ala Leu His Leu Gly Asp Thr Val Asp  
 130 135 140  
 35 Ser Asp Gln Phe Lys Arg Glu Glu Asp Phe Tyr Tyr Thr Glu Val Gln  
 145 150 155 160  
 Leu Lys Glu Glu Ser Ala Ala Ala Ala Ala Ala Ala Ala Asp Pro  
 165 170 175  
 40 Gln Ser Leu Gly Leu Pro Pro Pro Ser Gln Leu Pro Pro Pro Ala Xaa  
 180 185 190

45

50

## (2) INFORMATION FOR SEQ ID NO: 434:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

55 Met Ser Thr Asn Tyr Leu Thr Asp Val Cys Ser Leu Phe Ser Tyr Leu  
 1 5 10 15  
 60 Asn Tyr Leu Tyr Phe His His His Leu Pro Val Pro Asn Thr Xaa

584

20

25

30

## 5 (2) INFORMATION FOR SEQ ID NO: 435:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Gly Phe Phe Phe Val Leu Phe Phe Leu Tyr Leu Ala Leu Ser Arg  
 1 5 10 15  
 Asp Trp Ser Ile Asn Phe Leu Lys Asp His Arg Ile Asn Phe Phe Val  
 20 25 30  
 Ala Thr Ser Tyr Phe Ser Val Tyr Val Arg Gly Xaa Pro Xaa Val Pro  
 35 40 45  
 Ala Asp Thr Pro Leu Gly Pro Leu Leu Ser Leu Trp Leu His His Asn  
 50 55 60  
 Ala Phe Phe Ser Ile Leu Pro Lys Phe Pro Glu Asn Xaa Xaa Phe Leu  
 65 70 75 80  
 Ile Leu Lys Lys Leu Val Val Glu Met Gly Trp Asp Leu Phe Ile Ser  
 85 90 95  
 Pro Glu Asn Lys Xaa  
 100

35

## (2) INFORMATION FOR SEQ ID NO: 436:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Ala Arg Tyr Phe Ile Phe Phe Ile Leu Val Phe Met Lys Val Ser  
 1 5 10 15  
 Leu Asn Thr Thr Trp Pro Ala Pro Arg Pro Ala Thr Leu Arg Thr Ala  
 20 25 30  
 Asn Lys Ser Lys Xaa  
 35

55

## (2) INFORMATION FOR SEQ ID NO: 437:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

60 (B) TYPE: amino acid

(D) TOPOLOGY: linear

585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Phe Ser Thr Ile Arg Ser Gly Leu Thr Asp Arg Ser Val Asn Phe Leu  
 1 5 10 15

Phe Leu Phe Leu Asp Val Pro Asp Cys Arg Leu Val Asn Ile Glu Leu  
 20 25 30

Met Ala Asn Ser Thr Val Thr His Ala Xaa  
 35 40

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Leu  
 1

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Pro Trp Arg Arg Ala Gly Leu Met Met Leu Pro Ile Ile Thr Gly  
 1 5 10 15

Cys Cys Pro Cys Ser Ala Ser Ile Xaa  
 20 25

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Tyr Leu Cys Lys Thr Val Lys Val Leu Ile Cys Tyr Asp Trp Ile  
 1 5 10 15

Leu Gly Leu Val Ser Ser Gly Gln His Trp Val Val Ser Leu Ser Tyr  
 20 25 30

Ser Ile Arg Val Tyr Pro Ala Met His Phe Thr Leu Cys Val His Ile  
 35 40 45

Tyr Ser Lys Glu Pro Cys

586

50

## 5 (2) INFORMATION FOR SEQ ID NO: 441:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

Met Thr Ala Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys  
 1 5 10 15  
 Pro Ile Leu Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His  
 20 25 30  
 Ser Phe Ile His Ser Ser Asn Ile Cys Xaa  
 35 40

## 25 (2) INFORMATION FOR SEQ ID NO: 442:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Phe Leu Thr Thr Trp Phe Leu Leu Ser Val Ala Trp Xaa Ala  
 1 5 10 15  
 Leu Thr Arg Ser Gly Arg Ser Cys Leu Pro Leu Val Gly Arg Pro Arg  
 20 25 30  
 Glu Gln Ser Pro Arg Thr His Cys Ala Ala Ser Ser Thr Lys Glu Arg  
 35 40 45  
 Asn Ser Asp Pro Gln Pro Ser Pro Pro Glu Val Val Gly Pro Leu Trp  
 50 55 60  
 Ser Xaa  
 65

## 50 (2) INFORMATION FOR SEQ ID NO: 443:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Lys Ala Ile Gly Ile Glu Pro Ser Leu Ala Thr Tyr His His Ile  
 1 5 10 15  
 Ile Arg Leu Phe Asp Gln Pro Gly Asp Pro Leu Lys Arg Ser Ser Phe



587

20 25 30

Ile Ile Tyr Asp Ile Met Asn Glu Leu Met Gly Lys Arg Phe Ser Pro  
35 40 45

5 Lys Asp Pro Asp Asp Asp Lys Phe Phe Gln Ser Ala Met Ser Ile Cys  
50 55 60

10 Ser Ser Leu Arg Asp Leu Glu Leu Ala Tyr Gln Val His Gly Leu Leu  
65 70 75 80

Lys Thr Gly Asp Asn Trp Lys Phe Ile Gly Pro Asp Gln His Arg Asn  
85 90 95

15 Phe Tyr Tyr Ser Lys Phe Phe Asp Leu Ile Cys Leu Met Glu Gln Ile  
100 105 110

Asp Val Thr Leu Lys Trp Tyr Glu Asp Leu Ile Pro Ser Ala Tyr Phe  
115 120 125

20 Pro His Ser Gln Thr Met Ile His Leu Leu Gln Ala Leu Asp Val Ala  
130 135 140

25 Asn Arg Leu Glu Val Ile Pro Lys Ile Trp Glu Arg  
145 150 155

30 (2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr Leu Trp Gly Leu  
1 5 10 15

40 Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr Glu Glu Val Lys  
20 25 30

Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys  
35 40 45

45 Gly Asp Leu Leu Lys Cys Pro Leu Xaa  
50 55

50

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

60 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
1 5 10 15

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys  
 20 25 30  
 5 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg  
 35 40 45  
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His  
 50 55 60  
 10 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp  
 65 70 75 80  
 15 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr  
 85 90 95  
 Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln  
 100 105 110  
 20 Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp  
 115 120 125  
 Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu  
 130 135 140  
 25 His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe  
 145 150 155 160  
 30 Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr  
 165 170 175  
 Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu  
 180 185 190  
 35 Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met  
 195 200 205  
 Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu  
 210 215 220  
 40 Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met  
 225 230 235 240  
 45 Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe  
 245 250 255  
 Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn  
 260 265 270  
 50 Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys  
 275 280 285  
 Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met  
 290 295 300  
 55 Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg  
 305 310 315 320  
 60 Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser  
 325 330 335

589

Gln Xaa Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg  
 340 345 350

5 His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu  
 355 360 365

Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Ala Arg  
 370 375 380

10 Ala Trp Thr Thr Ser Thr Thr Cys Ser Arg Trp Ala Leu Arg Pro Pro  
 385 390 395 400

Arg Trp Thr Cys Ser Phe Leu Ser His Gly Val Ser Glu Gln Val Xaa  
 15 405 410 415

20

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Ala Pro Gly Pro Leu Ser Ala Thr Gln Ala Val Val Ile His Thr  
 1 5 10 15

Thr His Cys Leu Gln Leu Pro Val Trp Cys Leu Ser Leu Val Ser Glu  
 20 25 30

35 Leu Leu Gly Arg Ala Pro Pro His Asn Lys Asp Ala Leu Arg Pro Ser  
 35 40 45

40 Lys Lys Lys Lys Lys Lys Leu Xaa Gly Gly Pro Val Pro Ile Pro Pro  
 50 55 60

45

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

55 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser Pro  
 1 5 10 15

Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly Trp Ala  
 20 25 30

60

590

Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val  
 35 40 45

5 Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu  
 50 55 60

Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala Ala Val Arg Ser Xaa  
 65 70 75 80

10 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Xaa Gly Ala Ile  
 85 90 95

Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala  
 100 105 110

15 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe  
 115 120 125

His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met  
 130 135 140

Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val  
 145 150 155 160

25 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly  
 165 170 175

Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp  
 180 185 190

30 Lys Tyr Ser Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu Xaa  
 195 200 205

35

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

45

Met Ser Ser Leu Leu Ser Ala Gly Leu Gln Ala Ser Leu Cys Gly Lys  
 1 5 10 15

Xaa Leu Trp Ala Ser Thr Trp Tyr Leu Val Cys Cys Leu Leu Pro Phe  
 20 25 30

50

Phe His Gln Gly Cys Cys Asp His Lys Ser Lys Gln Gln Tyr Ile Pro  
 35 40 45

Asn Leu Lys Ser Tyr Cys Gly Leu Ser Thr Ile Glu Ile Xaa  
 50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 449:

60

(i) SEQUENCE CHARACTERISTICS:

591

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

5 Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile Leu Leu Val Phe  
1 5 10 15

10 Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala Pro Gly Pro Thr  
20 25 30

Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp Ala Arg Lys Asn  
35 40 45

15 His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro Asn His Cys Asp  
50 55 60

Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu Ile Glu Ala Asn  
65 70 75 80

20 Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His Met Glu Met Ser  
85 90 95

25 Pro Trp Phe Gln Phe Met Xaa Phe Ile Leu Gln Leu Asp Ile Ala Phe  
100 105 110

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val  
115 120 125

30 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala  
130 135 140

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys  
145 150 155 160

35 Thr Pro Glu His Gly Gly Pro Val Thr Met Asn Val Met Ser Phe Leu  
165 170 175

40 Ser Trp Lys Leu Gly Leu Trp Pro Met Lys Phe Tyr Leu Leu Asn Ile  
180 185 190

Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu  
195 200 205

45 Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr  
210 215 220

Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile  
225 230 235 240

50 Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro  
245 250 255

55 Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe  
260 265 270

Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp  
275 280 285

60 Met Leu Leu Phe Gly Asp Ile Arg Gln Ala Ser Ser Met Xaa Cys Phe

592

290                      295                      300

Xaa Pro Ser Gly Ser Ser Ser Val Ala Ser Thr Xaa  
305                      310                      315

5

(2) INFORMATION FOR SEQ ID NO: 450:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

15

Met Leu Ala Leu Leu Gly Leu Leu Ala Gly Thr Glu His Pro Pro Gly  
1                      5                      10                      15

20

Pro Gln Gly Pro Gly Pro Ser Xaa  
20

(2) INFORMATION FOR SEQ ID NO: 451:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Pro Ser Gly Ala Cys Cys Ser Pro Xaa  
1                      5                      10

35

(2) INFORMATION FOR SEQ ID NO: 452:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

45

Met Leu Pro Ala Leu Ser Thr Val Leu Leu Pro Thr Pro Ser Leu Cys  
1                      5                      10                      15

50

Ser Gly Asn Pro Arg Glu Gly Trp Ala Xaa  
20                      25

(2) INFORMATION FOR SEQ ID NO: 453:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

593

Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala Val Ile Cys Tyr  
 1 5 10 15

Leu Leu Gln Leu Leu Ser Gly Phe Ser Val Phe Leu Leu Pro Trp Ala  
 5 20 25 30

Pro Leu Ser Leu Arg Ala Phe Leu Met Pro Ile His Val Tyr Ser Gly  
 35 40 45

10 Ile Val Ile Phe Gly Thr Val Ile Ala Thr Ala Leu Met Gly Leu Thr  
 50 55 60

Glu Lys Leu Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser Thr Phe Pro  
 65 70 75 80

15 Pro Glu Gly Val Phe Val Asn Thr Leu Gly Leu Leu Ile Leu Val Phe  
 85 90 95

Gly Ala Leu Ile Phe Trp Ile Val Thr Arg Pro Gln Trp Lys Arg Pro  
 20 100 105 110

Lys Glu Pro Asn Ser Thr Ile Leu His Pro Asn Gly Gly Thr Glu Gln  
 115 120 125

25 Gly Ala Arg Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn Met Asp Lys  
 130 135 140

Ser Asp Ser Glu Leu Asn Xaa Glu Val Ala Ala Arg Lys Arg Asn Leu  
 145 150 155 160

30 Ala Leu Asp Glu Ala Gly Gln Arg Ser Thr Met Xaa  
 165 170

35 (2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 96 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Phe His Val Leu Met Ala Gln Val Thr Xaa Val Ile Ile Thr Thr  
 45 1 5 10 15

Val Ser Val Leu Val Phe Asp Phe Arg Pro Ser Leu Glu Phe Phe Leu  
 20 25 30

50 Glu Ala Xaa Ser Val Xaa Leu Ser Ile Phe Ile Tyr Asn Ala Ser Lys  
 35 40 45

Pro Gln Val Pro Glu Tyr Ala Pro Arg Gln Glu Arg Ile Arg Asp Leu  
 50 55 60

55 Ser Gly Asn Leu Trp Glu Arg Ser Ser Gly Asp Gly Glu Glu Leu Glu  
 65 70 75 80

Arg Leu Thr Lys Pro Lys Ser Asp Glu Ser Asp Glu Asp Thr Phe Xaa  
 85 90 95

5

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

15 Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln  
1 5 10 15

Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Val  
20 25 30

20 Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro  
35 40 45

25 Thr Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr  
50 55 60

His Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu  
65 70 75 80

30 Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro  
85 90 95

His Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu  
100 105 110

35 Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro  
115 120 125

40 Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp  
130 135 140

Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Xaa His  
145 150 155 160

45 Leu Gly Arg Lys Gln Gly Leu His Gly Asn Xaa  
165 170

50 (2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

60 Met Lys Ala Ser Gln Cys Cys Cys Cys Leu Ser His Leu Leu Ala Ser  
1 5 10 15



595

Val Leu Leu Leu Leu Leu Leu Pro Glu Leu Ser Gly Xaa Leu Xaa Val  
                     20                    25                    30

5 Leu Leu Gln Ala Ala Glu Ala Ala Pro Gly Xaa Gly Pro Pro Asp Pro  
                     35                    40                    45

Arg Pro Gly His Tyr Arg Arg Cys His Arg Ala Leu Thr Pro Ala Gln  
                     50                    55                    60

10 Gln Pro Gly Arg Gly Leu Ala Glu Ala Ala Gly Ala Ala Gly Leu Arg  
                     65                    70                    75                    80

Gly Arg Gln Trp Gln Gln Pro Cys Gly Arg Ala Xaa  
                     85                    90

15

(2) INFORMATION FOR SEQ ID NO: 457:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Ile Ser Val Leu Xaa Tyr Pro His Cys Val Val His Glu Leu Pro Glu  
   1                    5                    10                    15

Leu Thr Ala Glu Ser Leu Glu Ala Gly Asp Ser Asn Gln Phe Cys Trp  
   20                    25                    30

Arg Asn Leu Phe Ser Cys Ile Asn Leu Leu Arg Ile Leu Asn Lys Leu  
   35                    40                    45

Thr Lys Trp Lys His Ser Arg Thr Met Met Leu Val Val Phe Lys Ser  
   50                    55                    60

Ala Pro Ile Leu Lys Arg Ala Leu Lys Val Lys Gln Ala Met Met Gln  
   65                    70                    75                    80

40 Leu Tyr Val Leu Lys Leu Leu Lys Val Gln Thr Lys Tyr Leu Gly Arg  
                     85                    90                    95

Gln Trp Arg Lys Ser Asn Met Lys Thr Met Ser Ala Ile Tyr Gln Lys  
   100                    105                    110

45 Val Arg His Arg Leu Asn Asp Asp Trp Ala Tyr Gly Asn Asp Leu Asp  
                     115                    120                    125

50 Ala Arg Pro Trp Asp Phe Gln Ala Glu Glu Cys Ala Leu Arg Ala Asn  
                     130                    135                    140

Ile Glu Arg Phe Asn Ala Arg Arg Tyr Asp Arg Ala His Ser Asn Pro  
   145                    150                    155                    160

55 Asp Phe Leu Pro Val Asp Asn Cys Leu Gln Ser Val Leu Gly Gln Arg  
                     165                    170                    175

60 Val Asp Leu Pro Glu Asp Phe Gln Met Asn Tyr Asp Leu Trp Leu Glu  
                     180                    185                    190

Arg Glu Val Phe Ser Lys Pro Ile Ser Trp Glu Glu Leu Leu  
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

15

Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val  
 1 5 10 15

Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln  
 20 25 30

20

Gln Cys Ile Asn Glu Ala Xaa Xaa Val Lys Leu Ser Ser Pro Glu Arg  
 35 40 45

25

Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg  
 50 55 60

Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu  
 65 70 75 80

30

Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg  
 85 90 95

Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Xaa  
 100 105 110

35

Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu  
 115 120 125

40

His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp  
 130 135 140

Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp  
 145 150 155 160

45

Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp  
 165 170 175

Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala  
 180 185 190

50

Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met  
 195 200 205

55

Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala  
 210 215 220

Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln  
 225 230 235 240

60

Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu

597

245                      250                      255  
 Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg  
                          260                      265                      270  
 Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys  
                          275                      280                      285  
 Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr  
 10                      290                      295                      300  
 Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser Gly Pro  
 15                      305                      310                      315

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

25 Arg Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln  
       1                      5                      10                      15  
 Arg Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro  
                          20                      25                      30  
 30 Glu Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser  
                          35                      40                      45  
 Arg Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser  
 35                      50                      55                      60  
 Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr  
       65                      70                      75                      80  
 40 Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly  
                          85                      90                      95  
 Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu  
                          100                      105                      110  
 45 Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu  
                          115                      120                      125  
 Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu  
 50                      130                      135                      140  
 Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu  
       145                      150                      155                      160  
 55 Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala  
                          165                      170                      175  
 Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu  
                          180                      185                      190  
 60

598

Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn  
 195 200 205

5 Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn  
 210 215 220

Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile  
 225 230 235 240

10 Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln  
 245 250 255

Tyr Ala Pro Ser Ala  
 260

15

(2) INFORMATION FOR SEQ ID NO: 460:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

25 Met Lys Ala Ile Gly Ile Glu Pro Ser Leu Ala Thr Tyr His His Ile  
 1 5 10 15

Ile Arg Leu Phe Asp Gln Pro Gly Asp Pro Leu Lys Arg Ser Ser Phe  
 30 20 25 30

Ile Ile Tyr Asp Ile Met Asn Glu Leu Met Gly Lys Arg Phe Ser Pro  
 35 35 40 45

Lys Asp Pro Asp Asp Asp Lys Phe Phe Gln Ser Ala Met Ser Ile Cys  
 50 55 60

Ser Ser Leu Arg Asp Leu Glu Leu Ala Tyr Gln Val His Gly Leu Leu  
 65 70 75 80

40 Lys Thr Gly Asp Asn Trp Lys Phe Ile Gly Pro Asp Gln His Arg Asn  
 85 90 95

Phe Tyr Tyr Ser Lys Phe Phe Asp Leu Ile Cys Leu Met Glu Gln Ile  
 45 100 105 110

Asp Val Thr Leu Lys Trp Tyr Glu Asp Leu Ile Pro Ser Ala Tyr Phe  
 115 120 125

50 Pro His Ser Gln Thr Met Ile His Leu Leu Gln Ala Leu Asp Val Ala  
 130 135 140

Asn Arg Leu Glu Val Ile Pro Lys Ile Trp Glu Arg  
 145 150 155

55

(2) INFORMATION FOR SEQ ID NO: 461:

60 (i) SEQUENCE CHARACTERISTICS:

599

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

5  
 Lys Asp Ser Lys Glu Tyr Gly His Thr Phe Arg Ser Asp Leu Arg Glu  
 1 5 10 15  
 Glu Ile Leu Met Leu Met Ala Arg Asp Lys His Pro Pro Glu Leu Gln  
 10 20 25 30  
 Val Ala Phe Ala Asp Cys Ala Ala Asp Ile Lys Ser Ala Tyr Glu Ser  
 35 40 45  
 15 Gln Pro Ile Arg Gln Thr Ala Gln Asp Trp Pro Ala Thr Ser Leu Asn  
 50 55 60  
 Cys Ile Ala Ile Leu Phe Leu Arg Ala Gly Arg Thr Gln Glu Ala Trp  
 65 70 75 80  
 20 Lys Met Leu Gly Leu Phe Arg Lys His Asn Lys Ile Pro Arg Ser Glu  
 85 90 95  
 25 Leu Leu Asn Glu Leu Met Asp Ser Ala Lys Val Ser Asn Ser Pro Ser  
 100 105 110  
 Gln Ala Ile Glu Val Val Glu Leu Ala Ser Ala Phe Ser Leu Pro Ile  
 115 120 125  
 30 Cys Glu Gly Leu Thr Gln Arg Val Met Ser Asp Phe Ala Ile Asn Gln  
 130 135 140  
 Glu Gln Lys Glu Ala Leu Ser Asn Leu Thr Ala Leu Thr Ser Asp Ser  
 145 150 155 160  
 35 Asp Thr Asp Ser Ser Ser Asp Ser Asp Ser Asp Thr Ser Glu Gly Lys  
 165 170 175

40

(2) INFORMATION FOR SEQ ID NO: 462:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Ser Asp Asn Glu Ser Asp Ile Glu Asp Glu Asp Leu Lys Leu  
 1 5 10 15  
 55 Glu Leu Arg Arg Leu Arg Asp Lys His Leu Lys Glu Ile Gln Asp Leu  
 20 25 30  
 Gln Ser Arg Gln Lys His Glu Ile Glu Ser Leu Tyr Thr Lys Leu Gly  
 35 40 45  
 60

600

Lys Val Pro Pro Ala Val Ile Ile Pro Pro Ala Ala Pro Leu Ser Gly  
 50 55 60  
 Arg Arg Arg Arg Pro Thr Lys Ser Lys Gly Ser Lys Ser Ser Arg Ser  
 5 65 70 75 80  
 Ser Ser Leu Gly Asn Lys Ser Pro Gln Leu Ser Gly Asn Leu Ser Gly  
 85 90 95  
 10 Gln Ser Ala Ala Ser Val Leu His Pro Gln Gln Thr Leu His Pro Pro  
 100 105 110  
 Gly Asn Ile Pro Glu Ser Gly Gln Asn Gln Leu Leu Gln Pro Leu Lys  
 115 120 125  
 15 Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe Thr Ser Asp Gly  
 130 135 140  
 20 Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln Gly Thr Ser Ser  
 145 150 155 160  
 Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala Ala Gln Ala Gln  
 165 170 175  
 25 Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe Thr Asp Asp Leu  
 180 185 190  
 His Lys Leu Val Asp Asn Trp Ala Arg Asp Ala Met Asn Leu Ser Gly  
 195 200 205  
 30 Arg Arg Gly Ser Lys Gly His Met Asn Tyr Glu Gly Pro Gly Met Ala  
 210 215 220  
 35 Arg Lys Phe Ser Ala Pro Gly Gln Leu Cys Ile Ser Met Thr Ser Asn  
 225 230 235 240  
 Leu Gly Gly Ser Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly  
 245 250 255  
 40 His Phe Thr Lys Ser Met Cys Pro Pro Gln Gln Tyr Gly Phe Pro Ala  
 260 265 270  
 Thr Pro Phe Gly Ala Gln Trp Ser Gly Thr Gly Gly Pro Ala Pro Gln  
 275 280 285  
 45 Pro Leu Gly Gln Phe Gln Pro Val Gly Thr Ala Ser Leu Gln Asn Phe  
 290 295 300  
 50 Asn Ile Ser Asn Leu Gln Lys Ser Ile Ser Asn Pro Pro Gly Ser Asn  
 305 310 315 320  
 Leu Arg Thr Thr

55

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 133 amino acids

601

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

5 Ile Gln Asp Leu Gln Ser Arg Gln Lys His Glu Ile Glu Ser Leu Tyr  
 1 5 10 15

Thr Lys Leu Gly Lys Val Pro Pro Ala Val Ile Ile Pro Pro Ala Ala  
 20 25 30

10 Pro Leu Ser Gly Arg Arg Arg Arg Pro Thr Lys Ser Lys Gly Ser Lys  
 35 40 45

15 Ser Ser Arg Ser Ser Ser Leu Gly Asn Lys Ser Pro Gln Leu Ser Gly  
 50 55 60

Asn Leu Ser Gly Gln Ser Ala Ala Ser Val Leu His Pro Gln Gln Thr  
 65 70 75 80

20 Leu His Pro Pro Gly Asn Ile Pro Glu Ser Gly Gln Asn Gln Leu Leu  
 85 90 95

Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe  
 100 105 110

25 Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln  
 115 120 125

30 Gly Thr Ser Ser Thr  
 130

(2) INFORMATION FOR SEQ ID NO: 464:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln  
 1 5 10 15

45 Gly Thr Ser Ser Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala  
 20 25 30

Ala Gln Ala Gln Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe  
 35 40 45

50 Thr Asp Asp Leu His  
 50

55

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

60

602

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

5 Lys Gly His Met Asn Tyr Glu Gly Pro Gly Met Ala Arg Lys Phe Ser  
 1 5 10 15

Ala Pro Gly Gln Leu Cys Ile Ser Met Thr Ser Asn Leu Gly Gly Ser  
 20 25 30

10 Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly His Phe Thr Lys  
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 466:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe  
 1 5 10 15

30 Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly  
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Val Arg Val Ala Ala Glu Ser Met Xaa Leu Leu Leu Glu Cys Ala  
 1 5 10 15

45 Xaa Val Arg Gly Pro Glu Tyr Leu Thr Gln Met Trp His Phe Met Cys  
 20 25 30

Asp Ala Leu Ile Lys Ala Ile Gly Thr Glu Pro Asp Ser Asp Val Leu  
 35 40 45

50 Ser Glu Ile Met His Ser Phe Ala Lys  
 50 55

55

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

60

(B) TYPE: amino acid



603

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

5 Met Glu Ile Asn Asn Gln Asn Cys Phe Ile Val Ile Asp Leu Val Arg  
1 5 10 15

Thr Val Met Glu Asn Gly Val Glu Gly Leu Leu Ile Phe Gly Ala Phe  
20 25 30

10 Leu Pro Glu Ser Trp Leu Ile Gly Val Arg Cys Ser Ser Glu Pro Pro  
35 40 45

Lys Ala Leu Leu Leu Ile Leu Ala His Ser Gln Lys Arg Arg Leu Asp  
50 55 60

15 Gly Trp Ser Phe Ile Arg His Leu Arg Val His Tyr Cys Val Ser Leu  
65 70 75 80

20 Thr Ile His Phe Ser  
85

(2) INFORMATION FOR SEQ ID NO: 469:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Gln Asp Lys His Ala Glu Glu Val Arg Lys Asn Lys Glu Leu Lys Glu  
1 5 10 15

35 Glu Ala Ser Arg  
20

40

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

Gln Gln Asp Leu Ser Pro Trp Ala Ala Pro Val Gly Cys Pro Leu Xaa  
1 5 10 15

50 Xaa Ala Ser Xaa Thr Cys His Xaa Leu Pro Leu Ser Gly Cys Leu Arg  
20 25 30

55 Arg Gln Ser Xaa Ser Leu Pro Val Val Ala Xaa Leu Cys Phe Trp Phe  
35 40 45

Ser Cys Pro Leu Ala Ser Leu Phe Val Pro Gly Gln Pro Cys Val Thr  
50 55 60

60 Cys Pro Phe Pro Ser Leu Pro Phe Gln Asp Lys His Ala Glu Glu Val

604

Arg Lys Asn Lys Glu Leu Lys Glu Glu Ala Ser Arg

5

(2) INFORMATION FOR SEQ ID NO: 471:

10

(1) SEWING CHARACTERISTICS:

(2) LENGTH: 37 amino acids

(2) TYPE: amino acid

(D) TOPOLOGY: linear

2. SEQUENCE DESCRIPTION: SEQ ID NO: 471:

15

```
Pro Thr Arg Cys Cys Thr Thr Gln Pro Cys Arg Ser Ser Ala Arg Arg
      5              10             15
```

20

Pro Cys Trp Val Pro Met Val Pro Ser Pro Glu Gly Arg Glu Xaa Gln  
20 25 30

Two Two One Two Six  
21

25

(2) DEFINITION: FOR SEQ ID NO: 472:

30

(2) SEQUENCE CHARACTERISTICS:

(2) LENGTH: 363 amino acids

(E) TYPE: amino acid

(E) TCPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 472:

35

Met Lys Arg Ser Leu Asn Glu Asn Ser Ala Arg Ser Thr Ala Gly Cys  
1 5 10 15

Leu Pro Val Pro Leu Phe Asn Gln Lys Lys Arg Asn Arg Gln Pro Leu  
20 25 30

40

Thr Ser Asn Pro Leu Lys Asp Asp Ser Gly Ile Ser Thr Pro Ser Asp  
33 40 45

45

Asn Tyr Asp Phe Pro Pro Leu Pro Thr Asp Trp Ala Trp Glu Ala Val  
30 55 60

Asn	Pro	Gln	Val	Ala	Pro	Val	Met	Lys	Thr	Val	Asp	Thr	Gly	Gln	Ile
65					70					75					80

50

Pro His Ser Val Ser Arg Pro Leu Arg Ser Gln Asp Ser Val Phe Asn  
85 90 95

Ser Ile Gln Ser Asn Thr Gly Arg Ser Gln Gly Gly Trp Ser Tyr Arg  
100 105 110

55

Asp Gly Asn Lys Asn Thr Ser Leu Lys Thr Trp Xaa Lys Asn Asp Phe  
115 120 125

60

Lys Pro Glu Cys Lys Arg Thr Asn Leu Val Ala Asn Asp Gly Lys Asn  
133 135 140

605

Ser Cys Pro Met Ser Ser Gly Ala Gln Gln Gln Lys Gln Leu Arg Thr  
 145 150 155 160  
 5 Pro Glu Pro Pro Asn Leu Ser Arg Asn Lys Glu Thr Glu Leu Leu Arg  
 165 170 175  
 Gln Thr His Ser Ser Lys Ile Ser Gly Cys Thr Met Arg Gly Leu Asp  
 180 185 190  
 10 Lys Asn Ser Ala Leu Gln Thr Leu Lys Pro Asn Phe Gln Gln Asn Gln  
 195 200 205  
 Tyr Lys Xaa Gln Met Leu Asp Asp Ile Pro Glu Asp Asn Thr Leu Lys  
 210 215 220  
 Glu Thr Ser Leu Tyr Gln Leu Gln Phe Lys Glu Lys Ala Ser Ser Leu  
 225 230 235 240  
 20 Arg Ile Ile Ser Ala Val Ile Glu Ser Met Lys Tyr Trp Arg Glu His  
 245 250 255  
 Ala Gln Lys Thr Val Leu Leu Phe Glu Val Leu Ala Val Leu Asp Ser  
 260 265 270  
 25 Ala Val Thr Pro Gly Pro Tyr Tyr Ser Lys Thr Phe Leu Met Arg Asp  
 275 280 285  
 Gly Lys Asn Thr Leu Pro Cys Val Phe Tyr Glu Ile Asp Arg Glu Leu  
 290 295 300  
 Pro Arg Leu Ile Arg Gly Arg Val His Arg Cys Val Gly Asn Tyr Asp  
 305 310 315 320  
 35 Gln Lys Lys Asn Ile Phe Gln Cys Val Ser Val Arg Pro Ala Ser Val  
 325 330 335  
 Ser Glu Gln Lys Thr Phe Gln Ala Phe Val Lys Ile Ala Asp Val Glu  
 340 345 350  
 40 Met Gln Tyr Tyr Ile Asn Val Met Asn Glu Thr  
 355 360

45

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

55

Ser Gln Asp Ser Val Phe Asn Ser Ile Gln Ser Asn Thr Gly Arg Ser  
 1 5 10 15

Gln Gly Gly Trp Ser Tyr Arg Asp Gly Asn Lys Asn Thr Ser Leu Lys  
 20 25 30

60

Thr Trp Xaa Lys Asn Asp Phe Lys Pro Gln Cys Lys Arg

606

35

40

45

5 (2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Asn Lys Glu Thr Glu Leu Leu Arg Gln Thr His Ser Ser Lys Ile Ser  
1 5 10 15

15 Gly Cys Thr Met Arg Gly Leu Asp Lys Asn Ser Ala Leu Gln Thr Leu  
20 25 30

20 Lys Pro Asn Phe  
35

25 (2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Ser Ser Leu Arg Ile Ile Ser Ala Val Ile Glu Ser Met Lys Tyr Trp  
1 5 10 15

35 Arg Glu His Ala Gln Lys Thr Val Leu Leu Phe Glu Val Leu Ala Val  
20 25 30

40 Leu Asp Ser Ala Val Thr Pro Gly Pro Tyr Tyr Ser Lys Thr Phe Leu  
35 40 45

Met

45 (2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

55 Pro Arg Leu Ile Arg Gly Arg Val His Arg Cys Val Gly Asn Tyr Asp  
1 5 10 15

Gln Lys Lys Asn Ile Phe Gln Cys Val Ser Val Arg Pro Ala Ser Val  
20 25 30

60 Ser Glu Gln Lys Thr Phe Gln Ala Phe Val

35

40

## 5 (2) INFORMATION FOR SEQ ID NO: 477:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

Gly Val Phe Arg Pro Cys Val Cys Gly Arg Pro Ala Ser Leu Thr Cys  
 1 5 10 15  
 Ser Pro Leu Asp Pro Glu Val Gly Pro Tyr Cys Asp Thr Pro Thr Met  
 20 25 30  
 Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro Val  
 35 40 45  
 His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys Thr  
 50 55 60  
 Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg Gly  
 65 70 75 80  
 Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His Arg  
 85 90 95  
 Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp Val  
 100 105 110  
 Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr Lys  
 115 120 125  
 Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln Leu  
 130 135 140  
 Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp Val  
 145 150 155 160  
 Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu His  
 165 170 175  
 Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg  
 180 185 190  
 Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr Val  
 195 200 205  
 Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu Val  
 210 215 220  
 Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met Leu  
 225 230 235 240  
 Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu Leu  
 245 250 255

60

608

Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met Phe  
 260 265 270

5 Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe Ser  
 275 280 285

Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn Ala  
 290 295 300

10 Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys Xaa  
 305 310 315 320

Lys Trp Arg Thr Lys Ser Ser Trp Gly Ser Thr Ser Met Xaa Trp Thr  
 325 330 335

15 Xaa Arg Xaa Pro Xaa Asp Ala Arg Xaa Pro Val Val Gly Xaa Arg Xaa  
 340 345 350

20 Ile Gln Xaa Leu Lys Asp His Xaa Pro Arg Met Val Leu Asp Ser Lys  
 355 360 365

Pro Gln  
 370

25

(2) INFORMATION FOR SEQ ID NO: 478:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

35 Thr Cys Ser Pro Leu Asp Pro Glu Val Gly Pro Tyr Cys Asp Thr Pro  
 1 5 10 15

Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser  
 20 25 30

40 Pro Val His Thr Thr Leu Ser  
 35

45

(2) INFORMATION FOR SEQ ID NO: 479:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

55 Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His Arg  
 1 5 10 15

Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp Val  
 20 25 30

60 Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr Lys

35

40

45

Val Phe Gly Ser Lys Phe

50

5

(2) INFORMATION FOR SEQ ID NO: 480:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

15

Arg Glu Met Phe Glu Val Thr Gly Leu His Asp Val Asp Gln Gly Trp  
 1 5 10 15

20

Met Arg Ala Val Arg Lys His Ala Lys Gly Leu His Ile Val Pro Arg  
 20 25 30

Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp  
 35 40 45

25

Ser Glu Asp Glu  
 50

30

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

35

His Phe Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln  
 1 5 10 15

40

Lys Arg Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu  
 20 25 30

45

His Gln Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr  
 35 40 45

Pro Gly Thr Asp Gln Leu Gly Met  
 50 55

50

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

55

60

Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro

610

1                      5                      10                      15  
 Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu  
                          20                      25                      30  
 5 Asp Pro Lys Xaa Lys Trp Arg Thr Lys Ser Ser Trp Gly Ser Thr  
                          35                      40                      45

10

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

20 Glu Arg Gly Val Ser Ile Asn Gln Phe Cys Lys Glu Phe Asn Glu Arg  
      1                      5                      10                      15  
 Thr Lys Asp Ile Lys Glu Gly Ile Pro Leu Pro Thr Lys Ile Leu Val  
                          20                      25                      30  
 25 Lys Pro Asp Arg Thr Phe Glu Ile Lys Ile Gly Gln Pro Thr Val Ser  
                          35                      40                      45  
 Tyr Phe Leu Lys Ala Ala Ala Gly Ile Glu Lys Gly Ala Arg Gln Thr  
                          50                      55                      60  
 30 Gly Lys Glu Val Ala Gly Leu Val Thr Leu Lys His Val Tyr Glu Ile  
                          65                      70                      75                      80  
 Ala Arg Ile Lys Ala Gln Asp Glu Ala Phe Ala Leu Gln Asp Val Pro  
                          85                      90                      95  
 35 Leu Ser Ser Val Val Arg Ser Ile Ile Gly Ser Ala Arg Ser Leu Gly  
                          100                      105                      110  
 40 Ile Arg Val Val Lys Asp Leu Ser Ser Glu Glu Leu Ala Ala Phe Gln  
                          115                      120                      125  
 Lys Glu Arg Ala Ile Phe Leu Ala Ala Gln Lys Glu Ala Asp Leu Ala  
                          130                      135                      140  
 45 Ala Gln Glu Glu Ala Ala Lys Lys  
                          145                      150

50

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

60 Ala Val Tyr Thr Tyr His Glu Lys Lys Lys Asp Thr Ala Ala Ser Gly  
      1                      5                      10                      15



611

Tyr Gly Thr Gln Asn Ile Arg Leu Ser Arg Asp Ala Val Lys Asp Phe  
 20 25 30  
 5 Asp Cys Cys Cys Leu Ser Leu Gln Pro Cys His Asp Pro Val Val Thr  
 35 40 45  
 Pro Asp Gly Tyr Leu Tyr Glu Arg Glu Ala Ile Leu Glu Tyr Ile Leu  
 50 55 60  
 10 His Gln Lys Lys Glu Ile Ala Arg Gln Met Lys Ala Tyr Glu Lys Gln  
 65 70 75 80  
 Arg Gly Thr Arg Arg Glu Glu Gln Lys Glu Leu Gln Arg Ala Ala Ser  
 85 90 95  
 15 Gln Asp His Val Arg Gly Phe Leu Glu Lys Glu Ser Ala Ile Val Ser  
 100 105 110  
 Arg Pro Leu Asn Pro Phe Thr Ala Lys Ala Leu Ser Gly Thr Ser Pro  
 115 120 125  
 Asp Asp Val Gln Pro Gly Pro Ser Val Gly Pro Pro Ser Lys Asp Lys  
 130 135 140  
 25 Asp Lys Val Leu Pro Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala  
 145 150 155 160  
 Lys Ala Thr Lys Leu Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met  
 165 170 175  
 30 Ser Gly Lys Pro Leu Arg Met Ser Asp Leu Thr Pro Val His Phe Thr  
 180 185 190  
 Pro Leu Asp Ser Ser Val Asp Arg Val Gly Leu Ile Thr Arg Ser Glu  
 195 200 205  
 Arg Tyr Val Cys Ala Val Thr Arg Asp Ser Leu Ser Asn Ala Thr Pro  
 210 215 220  
 40 Cys Ala Val Leu Arg Pro Ser Gly Ala Val Val Thr Leu Glu Cys Val  
 225 230 235 240  
 Glu Lys Leu Ile Arg Lys Asp Met Val Asp Pro Val Thr Gly Asp Lys  
 245 250 255  
 45 Leu Thr Asp Arg Asp Ile Ile Val Leu Gln Arg Gly Gly Thr  
 260 265 270  
 50

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

60 Tyr Leu Tyr Glu Arg Glu Ala Ile Leu Glu Tyr Ile Leu His Gln Lys.

612

1                      5                      10                      15  
 Lys Glu Ile Ala Arg Gln Met Lys Ala Tyr Glu Lys Gln Arg Gly Thr  
                     20                      25                      30  
 5 Arg Arg Glu Glu Gln Lys Glu Leu Gln Arg Ala Ala Ser Gln Asp His  
                     35                      40                      45  
 10 Val Arg Gly Phe Leu Glu  
                     50

15 (2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Phe Thr Ala Lys Ala Leu Ser Gly Thr Ser Pro Asp Asp Val Gln Pro  
   1                      5                      10                      15  
 25 Gly Pro Ser Val Gly Pro Pro Ser Lys Asp Lys Asp Lys Val Leu Pro  
                     20                      25                      30  
 Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala Lys Ala Thr Lys Leu  
                     35                      40                      45  
 30 Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met Ser Gly Lys Pro Leu  
                     50                      55                      60

35

40 (2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Val His Phe Thr Pro Leu Asp Ser Ser Val Asp Arg Val Gly Leu Ile  
   1                      5                      10                      15  
 50 Thr Arg Ser Glu Arg Tyr Val Cys Ala Val Thr Arg Asp Ser Leu Ser  
                     20                      25                      30  
 Asn Ala Thr Pro Cys Ala Val Leu Arg Pro Ser Gly Ala Val Val Thr  
                     35                      40                      45  
 55 Leu Glu Cys Val Glu Lys Leu Ile  
                     50                      55

60

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

5  
 10 Met Asp Thr Ser Glu Asn Arg Pro Glu Asn Asp Val Pro Glu Pro Pro  
 1 5 10 15  
 Met Pro Ile Ala Asp Gln Val Ser Asn Asp Asp Arg Pro Glu Gly Ser  
 20 25 30  
 15 Val Glu Asp Glu Glu Lys Lys Glu Ser Ser Leu Pro Lys Ser Phe Lys  
 35 40 45  
 Arg Lys Ile Ser Val Val Ser Ala Thr Lys Gly Val Pro Ala Gly Asn  
 50 55 60  
 20 Ser Asp Thr Glu Gly Gly Gln Pro Gly Arg Lys Arg Arg Trp Gly Ala  
 65 70 75 80  
 Ser Thr Ala Thr Thr Gln Lys Lys Pro Ser Ile Ser Ile Thr Thr Glu  
 85 90 95  
 25 Ser Leu Lys Ser Leu Ile Pro Asp Ile Lys Pro Leu Ala Gly Gln Glu  
 100 105 110  
 30 Ala Val Val Asp Leu His Ala Asp Asp Ser Arg Ile Ser Glu Asp Glu  
 115 120 125  
 Thr Glu Arg Asn Gly Asp Asp Gly Thr His Asp Lys Gly Leu Lys Ile  
 130 135 140  
 35 Cys Arg Thr Val Thr Gln Val Val Pro Ala Glu Gly Gln Glu Asn Gly  
 145 150 155 160  
 Gln Arg Glu Glu Glu Glu Glu Lys Glu Pro Glu Ala Glu Pro Pro  
 165 170 175  
 40 Val Pro Pro Gln Val Ser Val Glu Val Ala Leu Pro Pro Pro Ala Glu  
 180 185 190  
 45 His Glu Val Lys Lys Val Thr Leu Gly Asp Thr Leu Thr Arg Arg Ser  
 195 200 205  
 Ile Ser Gln Gln Lys Ser Gly Val Ser Ile Thr Ile Asp Asp Pro Val  
 210 215 220  
 50 Arg Thr Ala Gln Val Pro Ser Pro Pro Arg Gly Lys Ile Ser Asn Ile  
 225 230 235 240  
 Val His Ile Ser Asn Leu Val Arg Pro Phe Thr Leu Gly Gln Leu Lys  
 245 250 255  
 55 Glu Leu Leu Gly Arg Thr Gly Thr Leu Val Glu Glu Ala Phe Trp Ile  
 260 265 270  
 60 Asp Lys Ile Lys Ser His Cys Phe Val Thr Tyr Ser Thr Val Glu Glu

614

275                      280                      285  
 Ala Val Ala Thr Arg Thr Ala Leu His Gly Val Lys Trp Pro Gln Ser  
 290                      295                      300  
 5 Asn Pro Lys Phe Leu Cys Ala Asp Tyr Ala Glu Gln Asp Glu Leu Asp  
 305                      310                      315                      320  
 10 Tyr His Arg Gly Leu Leu Val Asp Arg Pro Ser Glu Thr Lys Thr Glu  
 325                      330                      335  
 Glu Gln Gly Ile Pro Arg Pro Leu His Pro Pro Pro Pro Pro Pro Val  
 340                      345                      350  
 15 Gln Pro Pro Gln His Pro Arg Ala Glu Gln Arg Glu Gln Glu Arg Ala  
 355                      360                      365  
 Val Arg Glu Gln Trp Ala Glu Arg Glu Arg Glu Met Glu Arg Arg Glu  
 370                      375                      380  
 20 Arg Thr Arg Ser Glu Arg Glu Trp Asp Arg Asp Lys Val Arg Glu Gly  
 385                      390                      395                      400  
 Pro Arg Ser Arg Ser Arg Ser Arg Xaa Arg Arg Arg Lys Glu Arg Ala  
 405                      410                      415  
 25 Lys Ser Lys Glu Lys Lys Ser Glu Lys Lys Glu Lys Ala Gln Glu Glu  
 420                      425                      430  
 30 Pro Pro Ala Lys Leu Leu Asp Asp Leu Phe Arg Lys Thr Lys Ala Ala  
 435                      440                      445  
 Pro Cys Ile Tyr Trp Leu Pro Leu Thr Asp Ser Gln Ile Val Gln Lys  
 450                      455                      460  
 35 Glu Ala Glu Arg Ala Glu Arg Ala Lys Glu Arg Glu Lys Arg Arg Lys  
 465                      470                      475                      480  
 Glu Gln Glu Glu Glu Glu Gln Lys Glu Arg Glu Lys Glu Ala Glu Arg  
 485                      490                      495  
 40 Glu Arg Asn Arg Gln Leu Glu Arg Glu Lys Arg Arg Glu His Ser Arg  
 500                      505                      510  
 45 Glu Arg Asp Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Arg Gly Asp  
 515                      520                      525  
 Arg Asp Arg Asp Arg Glu Arg Asp Arg Glu Arg Gly Arg Glu Arg Asp  
 530                      535                      540  
 50 Arg Arg Asp Thr Lys Arg His Ser Arg Ser Arg Ser Arg Ser Thr Pro  
 545                      550                      555                      560  
 55 Val Arg Asp Arg Gly Gly Arg  
 565

(2) INFORMATION FOR SEQ ID NO: 489:

60

615

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Gly Cys Asp Ser Cys Pro Pro His Leu Pro Arg Glu Ala Phe Ala Gln  
 1 5 10 15  
 Asp Thr Gln Ala Glu Gly Glu Cys Ser Ser Arg Ala Glu Arg Ala Asp  
 20 25 30  
 Met Cys Pro Asp Ala Pro Pro Ser Gln Glu Val Pro Glu Gly Pro Gly  
 35 40 45  
 Ala Ala Pro  
 50

20

## (2) INFORMATION FOR SEQ ID NO: 490:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

Pro Gln Leu Pro Ser Cys Gly Arg Pro Trp Pro Gly Thr Ala Ser Val  
 1 5 10 15  
 Phe Gln Ser His Thr Gln Gly Pro Arg Glu Asp Pro Asp Pro Cys Arg  
 20 25 30  
 Ala Gln Gly Ser Ala Gly Thr His Cys Pro Ile Ser Leu Ser Pro Pro  
 35 40 45  
 Arg Gln  
 50

40

## (2) INFORMATION FOR SEQ ID NO: 491:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

50

Pro Gly Phe Arg Gly Pro Ser Gly Ser Leu Gly Cys Ser Phe Phe Pro  
 1 5 10 15  
 Arg Ser Leu Gly Arg Val Leu Pro Pro Gly Cys Gln Arg Pro Gly Ala  
 20 25 30  
 His Ala Asp Ser Ser Pro Pro Pro Thr Pro  
 35 40

60

## (2) INFORMATION FOR SEQ ID NO: 492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

5  
 10 Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg Ala Ala Ser Cys  
     1                    5                    10                    15  
     Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys Gly Leu  
                     20                    25                    30  
 15 Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln Met Ser Ser Gln  
                     35                    40                    45  
 20 Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys  
                     50                    55                    60  
     Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys  
                     65                    70                    75                    80  
 25 Val Leu Leu Ser

## 30 (2) INFORMATION FOR SEQ ID NO: 493:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

35  
 40 Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg Ala Ala Ser Cys  
     1                    5                    10                    15  
     Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys Gly Leu  
                     20                    25                    30  
 45 Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln Met Ser Ser Gln  
                     35                    40                    45  
     Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys  
                     50                    55                    60  
 50 Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys  
                     65                    70                    75                    80  
     Val Leu Leu Ser Asp Ser Asn Leu His Asp  
                     85                    90  
 55

## (2) INFORMATION FOR SEQ ID NO: 494:

60 (i) SEQUENCE CHARACTERISTICS:

617

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

5

Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys Ala Ser Cys Pro  
 1 5 10 15

10

Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys Val Leu Leu Ser  
 20 25 30

Asp Ser

15

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

25

Ser Cys Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys  
 1 5 10 15

30

Gly Leu Ala Glu Glu Leu Glu Lys Glu  
 20 25

(2) INFORMATION FOR SEQ ID NO: 496:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

40

Ser Gln Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe  
 1 5 10 15

45

Arg Cys Ala Ser Cys  
 20

(2) INFORMATION FOR SEQ ID NO: 497:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Arg Glu Ala Gly Gln Asn Ser Glu Arg Gln Tyr Val Ser Leu Ser Arg  
 1 5 10 15

60

Asp

## 5 (2) INFORMATION FOR SEQ ID NO: 498:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

15 Glu Ser Ser Gly Gln Ala Arg Thr Leu Ala Asp Pro Gly Pro Gly Trp  
 1 5 10 15  
 20 Pro Arg Gln Gln Gly Met Cys Phe Gly Ser Leu Thr Gly Leu Ser Thr  
 20 20 25 30  
 Thr Pro His Gly Phe Leu Thr Val Ser Ala Glu Ala Asp Pro Arg Leu  
 20 35 40 45  
 Ile Glu Ser Leu Ser Gln Met Leu Ser Met Gly Phe Ser Asp Glu Gly  
 50 55 60  
 25 Gly Trp Leu Thr Arg Leu Leu Gln Thr Lys Asn Tyr Asp Ile Gly Ala  
 65 70 75 80  
 Ala Leu Asp Thr Ile Gln Tyr Ser Lys His  
 85 90

30

## (2) INFORMATION FOR SEQ ID NO: 499:

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

45 Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val  
 1 5 10 15  
 Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu  
 45 20 25 30  
 Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Xaa Ala Val Arg Ser His  
 35 40 45  
 50 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Ser Gly Ala Ile  
 50 55 60  
 Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala  
 65 70 75 80  
 55 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe  
 85 90 95  
 His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met  
 100 105 110

60



Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val  
 115 120 125  
 5 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly  
 130 135 140  
 Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Xaa Ser Thr Gly Trp  
 145 150 155  
 10

(2) INFORMATION FOR SEQ ID NO: 500:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:  
 20 Pro Arg Ser Arg Pro Ala Leu Arg Pro Gly Arg Gln Arg Pro Pro Ser  
 1 5 10 15  
 25 His Ser Ala Thr Ser Gly Val Leu Arg Pro Arg Lys Lys Pro Asp Pro  
 20 25 30  
 30

(2) INFORMATION FOR SEQ ID NO: 501:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:  
 40 Met Thr Leu Ile Thr Pro Ser Xaa Lys Leu Thr Phe Xaa Lys Gly Asn  
 1 5 10 15  
 Lys Ser Trp Ser Ser Arg Ala Cys Ser Ser Thr Leu Val Asp Pro  
 20 25 30  
 45

(2) INFORMATION FOR SEQ ID NO: 502:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:  
 55 Gly His Pro Ser Pro Ala Leu Ser Ile Ala Pro Ser Asp Gly Ser Gln  
 1 5 10 15  
 60 Leu Pro Cys Asp Glu Val Pro Tyr Gly Glu Ala His Val Thr Arg Tyr  
 20 25 30

620

Cys Lys Lys Pro Leu Thr Asn Ser His Leu Glu Thr Glu Ala Gln Ser  
 35 40 45

5 Ser Ser Leu  
 50

10 (2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

20 GCTTCGTGTC CAACCCCTCTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60  
 GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120  
 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180  
 25 TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTTTTA TTCTGTGGG GCTCACCCCA 240  
 AAGTATTAAA AGTAGCTTTG TAA 263

30

(2) INFORMATION FOR SEQ ID NO: 504:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

GCTTCGTGTC CAACCCCTCTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60  
 45 GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120  
 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180  
 TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTTTTA TTCTGTGGG GCTCACCCCA 240  
 50 AAGTATTAAA AGTAGCTTTG TAA 263

55

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
 60 (B) TYPE: nucleic acid

621

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

5  
 GCTTCGTGTC CAACCTCTTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60  
 GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120  
 10 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180  
 TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTTTTA TTCTGTGGG GCTCACCCCA 240  
 AAGTATTAAA AGTAGCTTTG TAA 263  
 15

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

20  
 TGGCTCACTG TCTTACAATC ACTGCTGTGG AATCATGATA CCACTTTTAG CTCTTTGCAT 60  
 30 CTTCCTTCAG TGTATTTTGG TTTTCAAGA GGAAGTAGAT TTAACTGGA CCACTTTGAG 120  
 TACTGACATC ATTGATAAAT AAAGTGGCTT GTGGTTTCAA 160  
 35

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

40  
 Leu Asp Glu Leu Met Ala His Leu Thr Glu Met Gln Ala Lys Val Ala  
 1 5 10 15  
 50 Val Arg Ala Asp Ala Gly Lys Lys His Leu Pro Asp Lys Gln Asp His  
 20 25 30  
 Lys Ala Ser Leu Asp Ser Met Leu Gly Gly Leu Glu Gln Glu Leu Gln  
 35 40 45  
 55 Asp Leu Gly Ile Ala Thr Val Pro Lys Gly His Cys Ala Ser Cys Gln  
 50 55 60  
 Lys Pro Ile Ala Gly Lys Val Ile His Ala Leu Gly Gln Ser Trp His  
 65 70 75 80  
 60

622

Pro Glu His Phe Val Cys Thr His Cys Lys Glu Glu Ile Gly Ser Ser  
85 90 95

5 Pro Phe Phe Glu Arg Ser Gly Leu Xaa Tyr Cys Pro Asn Asp Tyr His  
100 105 110

Gln Leu Phe Ser Pro Arg Cys Ala Tyr Cys Ala Ala Pro Ile Leu Asp  
115 120 125

10 Lys Val Leu Thr Ala Met Asn Gln Thr Trp His Pro Glu His Phe Phe  
130 135 140

Cys Ser His Cys Gly Glu Val Phe Gly Ala Glu Gly Phe His Glu Lys  
145 150 155 160

15 Asp Lys Lys Pro Tyr Cys Arg Lys Asp Phe Leu Ala Met Phe Ser Pro  
165 170 175

Lys Cys Gly Gly Cys Asn Arg Pro Val Leu Glu Asn Tyr Leu Ser Ala  
180 185 190

Met Asp Thr Val Trp His Pro Glu Cys Phe Val Cys Gly Asp Cys Phe  
195 200 205

25 Thr Ser Phe Ser Thr Gly Ser Phe Phe Glu Leu Asp Gly Arg Pro Phe  
210 215 220

Cys Glu Leu His Tyr His His Arg Arg Gly Thr Leu Cys His Gly Cys  
225 230 235 240

30 Gly Gln Pro Ile Thr Gly Arg Cys Ile Ser Ala Met Gly Tyr Lys Phe  
245 250 255

His Pro Glu His Phe Val Cys Ala Phe Cys Leu Thr Gln Leu Ser Lys  
260 265 270

Gly Ile Phe Arg Glu Gln Asn Asp Lys Thr Tyr Cys Gln Pro Cys Phe  
275 280 285

40 Asn Lys Leu Phe  
290

45 (2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Lys Ala Ser Leu Asp Ser Met Leu Gly Gly Leu Glu Gln Glu Leu Gln  
1 5 10 15

55 Asp Leu Gly Ile Ala Thr Val Pro Lys Gly His Cys Ala Ser Cys Gln  
20 25 30

Lys Pro Ile Ala Gly Lys Val Ile His Ala Leu  
35 40

## (2) INFORMATION FOR SEQ ID NO: 509:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Cys Pro Asn Asp Tyr His Gln Leu Phe Ser Pro Arg Cys Ala Tyr Cys  
 1 5 10 15  
 Ala Ala Pro Ile Leu Asp Lys Val Leu Thr Ala Met Asn Gln Thr Trp  
 20 25 30  
 His Pro Glu His Phe Phe Cys Ser His Cys Gly Glu Val Phe Gly Ala  
 35 40 45  
 Glu Gly  
 50

## (2) INFORMATION FOR SEQ ID NO: 510:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Asp Lys Lys Pro Tyr Cys Arg Lys Asp Phe Leu Ala Met Phe Ser Pro  
 1 5 10 15  
 Lys Cys Gly Gly Cys Asn Arg Pro Val Leu Glu Asn Tyr Leu Ser Ala  
 20 25 30  
 Met Asp Thr Val Trp His Pro Glu Cys Phe Val Cys Gly Asp Cys Phe  
 35 40 45  
 Thr Ser Phe Ser Thr Gly Ser Phe Phe Glu Leu Asp Gly Arg Pro Phe  
 50 55 60  
 Cys Glu Leu  
 65

## (2) INFORMATION FOR SEQ ID NO: 511:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Cys Gly Gln Pro Ile Thr Gly Arg Cys Ile Ser Ala Met Gly Tyr Lys  
 1 5 10 15

Phe His Pro Glu His Phe Val Cys Ala Phe Cys Leu Thr Gln Leu Ser  
20 25 30

5 Lys Gly Ile Phe Arg Glu Gln Asn Asp Lys Thr Tyr Cys Gln  
35 40 45

10 (2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Gly Ser Ser Gln Ser Val Glu Ile Pro Gly Gly Gly Thr Glu Gly  
1 5 10 15  
20 Tyr His Val Leu Arg Val Gln Glu Asn Ser Pro Gly His Arg Ala Gly  
20 25 30  
25 Leu Glu Pro Phe Phe Asp Phe Ile Val Ser Ile Asn Gly Ser Arg Leu  
35 40 45  
Asn Lys Asp Asn Asp Thr Leu Lys Asp Leu Leu Lys Xaa Asn Val Glu  
50 55 60  
30 Lys Pro Val Lys Met Leu Ile Tyr Ser Ser Lys Thr Leu Glu Leu Arg  
65 70 75 80  
Glu Thr Ser Val Thr Pro Ser Asn Leu Trp Gly Gly Gln Gly Leu Leu  
85 90 95  
35 Gly Val Ser Ile Arg Phe Cys Ser Phe Asp Gly Ala Asn Glu Asn Val  
100 105 110  
40 Trp His Val Leu Glu Val Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly  
115 120 125  
Leu Arg Pro His Ser Asp Tyr Ile Ile Gly Ala Asp Thr Val Met Asn  
130 135 140  
45 Glu Ser Glu Asp Leu Phe Ser Leu Ile Glu Thr His Glu Ala Lys Pro  
145 150 155 160  
Leu Lys Leu Tyr Val Tyr Asn Thr Asp Thr Asp Asn Cys Arg Glu Val  
165 170 175  
50 Ile Ile Thr Pro Asn Ser Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys  
180 185 190  
Gly Ile Gly Tyr Gly Tyr Leu His Arg Ile Pro Thr Arg Pro Phe Glu  
195 200 205  
55 Glu Gly Lys Lys Ile Ser Leu Pro Gly Gln Met Ala Gly Thr Pro Ile  
210 215 220  
60 Thr Pro Leu Lys Asp Gly Phe Thr Glu Val Gln Leu Ser Ser Val Asn

625

225                      230                      235                      240  
 Pro Pro Ser Leu Ser Pro Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu  
                                  245                      250                      255  
 5 Thr Gly Leu Ser Ile Ser Ser Thr Pro Pro Ala Val Ser Ser Val Leu  
                                  260                      265                      270  
 10 Ser Thr Gly Val Pro Thr Val Pro Leu Leu Pro Pro Gln Val Asn Gln  
                                  275                      280                      285  
 Ser Leu Thr Ser Val Pro Pro Met Asn Pro Ala Thr Thr Leu Pro Gly  
                                  290                      295                      300  
 15 Leu Met Pro Leu Pro Ala Gly Leu Pro Asn Leu Pro Asn Leu Asn Leu  
                                  305                      310                      315                      320  
 Asn Leu Pro Ala Pro His Ile Met Pro Gly Val Gly Leu Pro Glu Leu  
                                  325                      330                      335  
 20 Val Asn Pro Gly Leu Pro Pro Leu Pro Ser Met Pro Pro Arg Asn Leu  
                                  340                      345                      350  
 Pro Gly Ile Ala Pro Leu Pro Leu Pro Ser Glu Phe Leu Pro Ser Phe  
 25                      355                      360                      365  
 Pro Leu Val Pro Glu Ser Ser Ser Ala Ala Ser Ser Gly Glu Leu Leu  
                                  370                      375                      380  
 30 Ser Ser Leu Pro Pro Thr Ser Asn Ala Pro Ser Asp Pro Ala Thr Thr  
                                  385                      390                      395                      400  
 Thr Ala Lys Ala Asp Ala Ala Ser Ser Leu Thr Val Asp Val Thr Pro  
                                  405                      410                      415  
 35 Pro Thr Ala Lys Ala Pro Thr Thr Val Glu Asp Arg Val Gly Asp Ser  
                                  420                      425                      430  
 Thr Pro Val Ser Glu Lys Pro Val Ser Ala Ala Val Asp Ala Asn Ala  
 40                      435                      440                      445  
 Ser Glu Ser Pro  
                                  450

45

(2) INFORMATION FOR SEQ ID NO: 513:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

55

Ser Val Glu Ile Pro Gly Gly Gly Thr Glu Gly Tyr His Val Leu Arg  
   1                      5                      10                      15

60

Val Gln Glu Asn Ser Pro Gly His Arg Ala Gly Leu Glu Pro Phe Phe  
                                  20                      25                      30

626

Asp Phe Ile Val Ser Ile Asn Gly Ser Arg Leu Asn Lys Asp Asn Asp  
35 40 45

5 Thr Leu Lys Asp Leu Leu Lys Xaa Asn Val Glu Lys Pro Val Lys Met  
50 55 60

Leu Ile Tyr Ser Ser Lys Thr Leu Glu Leu Arg Glu Thr Ser Val Thr  
65 70 75 80

10 Pro Ser Asn Leu Trp Gly Gly Gln Gly Leu Leu Gly Val Ser Ile Arg  
85 90 95

15 Phe Cys Ser Phe Asp Gly Ala Asn Glu Asn Val Trp His  
100 105

(2) INFORMATION FOR SEQ ID NO: 514:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro His Ser Asp  
1 5 10 15

30 Tyr Ile Ile Gly Ala Asp Thr Val Met Asn Glu Ser Glu Asp Leu Phe  
20 25 30

Ser Leu Ile Glu Thr His Glu Ala Lys Pro Leu Lys Leu Tyr Val Tyr  
35 40 45

35 Asn Thr Asp Thr Asp Asn Cys Arg Glu Val Ile Ile Thr Pro Asn Ser  
50 55 60

Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr  
65 70 75 80

40 Leu His Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser  
85 90 95

45 Leu Pro Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly  
100 105 110

Phe Thr Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro  
115 120 125

50 Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser  
130 135 140

Ser  
145

55

(2) INFORMATION FOR SEQ ID NO: 515:

60 (i) SEQUENCE CHARACTERISTICS:



627

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

5

Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro His Ser Asp  
 1 5 10 15

10

Tyr Ile Ile Gly Ala Asp Thr Val Met Asn Glu Ser Glu Asp Leu Phe  
 20 25 30

Ser Leu Ile Glu Thr His Glu Ala Lys Pro Leu Lys Leu Tyr Val Tyr  
 35 40 45

15

Asn Thr Asp Thr Asp Asn Cys Arg Glu Val Ile Ile Thr Pro Asn Ser  
 50 55 60

Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr  
 65 70 75 80

20

Leu His Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser  
 85 90 95

25

Leu Pro Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly  
 100 105 110

Phe Thr Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro  
 115 120 125

30

Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser  
 130 135 140

Ser  
 145

35

(2) INFORMATION FOR SEQ ID NO: 516:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

45

Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser Leu Pro  
 1 5 10 15

50

Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly Phe Thr  
 20 25 30

Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro Pro Gly  
 35 40 45

55

Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser Ser Thr  
 50 55 60

Pro Pro Ala Val Ser Ser Val Leu Ser Thr Gly Val Pro Thr Val Pro  
 65 70 75 80

60

[illegible]

(2) INFORMATION FOR SEQ ID NO: 517:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

	Pro Gly Leu Pro Pro Ser Met Pro Pro Arg Asn Leu Pro Gly	
	1 5 10 15	
30	Ile Ala Pro Leu Pro Leu Pro Ser Glu Phe Leu Pro Ser Phe Pro Leu	
	20 25 30	
	Val Pro Glu Ser Ser Ser Ala Ala Ser Ser Gly Glu Leu Leu Ser Ser	
	35 40 45	
35	Leu Pro Pro Thr Ser Asn Ala Pro Ser Asp Pro Ala Thr Thr Thr Ala	
	50 55 60	
	Lys Ala Asp Ala Ala Ser Ser Leu Thr Val Asp Val Thr Pro Pro Thr	
40	65 70 75 80	
	Ala Lys Ala Pro Thr Thr Val Glu Asp Arg Val Gly Asp Ser Thr Pro	
	85 90 95	
45	Val Ser Glu Lys Pro Val Ser Ala Ala Val Asp Ala Asn	
	100 105	

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

60 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
1 5 10 15  
Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa

629

20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Trp Ile Phe Gly Val Leu His Val Val His  
35 40 45

5 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
50 55 60

10 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
65 70 75 80

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys  
85 90

15

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

25 Trp Ile Phe Gly Val Leu His Val Val His Ala Ser Val Val Thr Ala  
1 5 10 15

Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met Phe Ile Phe Leu  
20 25 30

30 Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu Tyr Tyr Arg Leu  
35 40 45

35 Phe Lys Asn Val Pro Cys Cys  
50 55

40

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Ala Leu Thr Arg Ile Pro Pro Gly Asp Trp Val Ile Asn Val Thr Ala  
1 5 10 15

50 Val Ser Phe Ala Gly Lys Thr Thr Ala Arg Phe Phe Xaa His Ser Ser  
20 25 30

Pro Pro Ser Leu Gly Asp Gln Ala Arg Thr Asp Pro Gly His Gln Arg  
35 40 45

55 Arg Asp  
50

60

630

## (2) INFORMATION FOR SEQ ID NO: 521:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Leu Gln Glu Val Asn Ile Thr Leu Pro Glu Asn Ser Val Trp Tyr Glu  
 1 5 10 15  
 Arg Tyr Lys Phe Asp Ile Pro Val Phe His Leu  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Gln Gly Ser Gly Ser Gln Phe Arg Ala Cys Leu Leu Cys Leu Cys  
 1 5 10 15  
 Phe Ser Cys Pro Cys Ser Pro Gly Gly Pro Arg Trp Asn Ser Arg Gln  
 20 25 30  
 Gly Gly Arg Arg Phe Pro Lys Thr Cys Arg Ala Ile Ser Gln Asn Leu  
 35 40 45  
 Val Phe Lys Tyr Lys Thr Phe Cys Pro Val Arg Tyr Met Gln Pro His  
 50 55 60  
 Arg Ser Ser Leu Cys Leu His Phe Thr Ser Tyr Val Phe Ile Leu Ser  
 65 70 75 80  
 Thr Trp Gly Ser Leu Arg Thr Tyr Ser Thr Asp Leu Lys Lys Lys Lys  
 85 90 95  
 Lys Asn Ser Arg Gly Gly Pro Val Pro Ile Arg Pro Lys Ser  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO: 523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

TAGCATGTAG CCAATCGAAT AACNTATAAG GACAAAGTGG AGTCCACGCG TGCGGCCGTC  
 TAGACTAGTG GATCCCCCGG CTGCAGGATT CGGCACGAG.

60

99

## 5 (2) INFORMATION FOR SEQ ID NO: 524:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Gln Gly Ser Gly Ser Gln Phe Arg Ala Cys Leu Leu Cys Leu Cys  
 1 5 10 15

15 Phe Ser Cys Pro Cys Ser Pro Gly Gly Pro Arg Trp Asn Ser Arg Gln  
 20 25 30

20 Gly Gly Arg Arg Phe Pro Lys Thr Cys Arg Ala Ile Ser Gln Asn Leu  
 35 40 45

Val Phe Lys  
 50

25

## (2) INFORMATION FOR SEQ ID NO: 525:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

35 Pro Val Arg Tyr Met Gln Pro His Arg Ser Ser Leu Cys Leu His Phe  
 1 5 10 15

Thr Ser Tyr Val Phe Ile Leu Ser Thr Trp Gly Ser Leu Arg Thr Tyr  
 20 25 30

40 Ser Thr Asp Leu Lys Lys Lys Lys Asn Ser Arg Gly Gly Pro Val  
 35 40 45

45 Pro Ile Arg Pro Lys Ser  
 50

## 50 (2) INFORMATION FOR SEQ ID NO: 526:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Gly Glu Glu Gln Arg Asp Cys Ser Leu Gly Trp Arg Gly Val Gly Met  
 1 5 10 15

60 Arg Ala Thr His Cys Gln Ala Ala Arg Met Phe Val Leu Phe Ser Leu

632

20 25 30

Pro Lys Tyr Ala Gly Leu  
35

5

(2) INFORMATION FOR SEQ ID NO: 527:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

15

Met Pro Arg Lys Thr Ser Lys Cys Arg Gln Leu Leu Cys Ser Gly Ala  
1 5 10 15

20

Ser Arg Asn Ala Asp Thr Ala Ala Arg Gln Ser Thr Cys Ser Ser His  
20 25 30

Arg Pro Pro Gly Lys Ile Pro Ser Leu Gly Pro Arg Arg Xaa Pro Gly  
35 40 45

25

Cys Xaa Ser Val Pro Ser Ser Arg Gly Glu Gln Ser Thr Gly Ser Pro  
50 55 60

Ala Ala Pro Arg Cys Gly Arg Arg Asp Ala His Arg Gly Leu Pro Gly  
65 70 75 80

30

Gly Ala Ala Met Thr Pro Gly Asp Thr Trp Ala Ser Phe Asn Pro Arg  
85 90 95

35

Ala Gly His Ser Lys Ser Gln Gly Glu Gly Gln Glu Ser Ser Gly Ala  
100 105 110

Ser Arg Gln Asp Arg His Pro Val Ser His Trp Val Glu Arg Gln Arg  
115 120 125

40

Glu Ala Trp Gly Ala Pro Arg Ser Ser Ser Ala Gly Gly Val Lys Val  
130 135 140

Ala Ala Thr Thr Glu Arg Glu Pro Glu Phe Lys Ile Lys Thr Gly Lys  
145 150 155 160

45

Ala

50

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

55

60

Cys Ser Gly Ala Ser Arg Asn Ala Asp Thr Ala Ala Arg Gln Ser Thr  
1 5 10 15

633

Cys Ser Ser His Arg Pro Pro Gly Lys Ile Pro Ser Leu Gly Pro Arg  
20 25 30

5 Arg Xaa Pro Gly Cys Xaa Ser Val Pro Ser Ser Arg Gly Glu Gln Ser  
35 40 45

Thr Gly Ser Pro Ala Ala Pro Arg Cys Gly Arg Arg Asp Ala His Arg  
50 55 60

10 Gly Leu Pro Gly Gly Ala Ala Met Thr Pro Gly Asp Thr Trp Ala Ser  
65 70 75 80

15 Phe Asn Pro Arg Ala Gly His Ser  
85

20 (2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Gln Gly Glu Gly Gln Glu Ser Ser Gly Ala Ser Arg Gln Asp Arg His  
1 5 10 15

30 Pro Val Ser His Trp Val Glu Arg Gln Arg Glu Ala Trp Gly Ala Pro  
20 25 30

Arg Ser Ser Ser Ala Gly Gly Val Lys Val Ala Ala Thr Thr Glu Arg  
35 40 45

Glu Pro Glu Phe Lys Ile Lys Thr Gly Lys Ala  
50 55

40 (2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 235 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

50 Met Ser Pro Arg Tyr Pro Gly Gly Pro Arg Pro Pro Leu Arg Ile Pro  
1 5 10 15

Asn Gln Ala Leu Gly Gly Val Pro Gly Ser Gln Pro Leu Leu Pro Ser  
20 25 30

55 Gly Met Asp Pro Thr Arg Gln Gln Gly His Pro Asn Met Gly Gly Pro  
35 40 45

Met Gln Arg Met Thr Pro Pro Arg Gly Met Val Pro Leu Gly Pro Gln  
50 55 60

60

634

Asn Tyr Gly Gly Ala Met Arg Pro Pro Leu Asn Ala Leu Gly Gly Pro  
 65 70 75 80  
 Gly Met Pro Gly Met Asn Met Gly Pro Gly Gly Gly Arg Pro Trp Pro  
 5 85 90 95  
 Asn Pro Thr Asn Ala Asn Ser Ile Pro Tyr Ser Ser Ala Ser Pro Gly  
 100 105 110  
 10 Asn Tyr Val Gly Pro Pro Gly Gly Gly Gly Pro Pro Gly Thr Pro Ile  
 115 120 125  
 Met Pro Ser Pro Ala Asp Ser Thr Asn Ser Gly Asp Asn Met Tyr Thr  
 130 135 140  
 15 Leu Met Asn Ala Val Pro Pro Gly Pro Asn Arg Pro Asn Phe Pro Met  
 145 150 155 160  
 Gly Pro Gly Ser Asp Gly Pro Met Gly Gly Leu Gly Gly Met Glu Ser  
 20 165 170 175  
 His His Met Asn Gly Ser Leu Gly Ser Gly Asp Met Asp Ser Ile Ser  
 180 185 190  
 25 Lys Asn Ser Pro Asn Asn Met Ser Leu Ser Asn Gln Pro Gly Thr Pro  
 195 200 205  
 Arg Asp Asp Gly Glu Met Gly Gly Asn Phe Leu Asn Pro Phe Gln Ser  
 210 215 220  
 30 Glu Ser Tyr Ser Pro Ser Met Thr Met Ser Val  
 225 230 235

35

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

45 Met Ser Pro Arg Tyr Pro Gly Gly Pro Arg Pro Pro Leu Arg Ile Pro  
 1 5 10 15  
 Asn Gln Ala Leu Gly Gly Val Pro Gly Ser Gln Pro Leu Leu Pro Ser  
 20 25 30  
 50 Gly Met Asp Pro Thr Arg Gln Gln Gly His Pro Asn Met Gly Gly Pro  
 35 40 45  
 Met Gln Arg Met Thr Pro Pro Arg Gly Met Val Pro Leu Gly Pro Gln  
 50 55 60  
 55 Asn Tyr Gly Gly Ala Met Arg Pro Pro Leu Asn Ala Leu Gly Gly Pro  
 65 70 75 80  
 60 Gly Met Pro Gly Met Asn Met Gly Pro Gly Gly Gly Arg Pro Trp Pro  
 85 90 95



635

Asn Pro Thr Asn Ala Asn Ser Ile Pro Tyr Ser Ser Ala Ser Pro Gly  
 100 105 110

5 Asn Tyr

10 (2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Leu Asn Ala Leu Gly Gly Pro Gly Met Pro Gly Met Asn Met Gly Pro  
 1 5 10 15

20

Gly Gly Gly Arg Pro Trp Pro Asn Pro Thr Asn Ala Asn Ser Ile Pro  
 20 25 30

25

Tyr Ser Ser Ala Ser Pro Gly Asn Tyr Val Gly Pro Pro Gly Gly Gly  
 35 40 45

Gly Pro Pro Gly Thr Pro Ile Met Pro Ser Pro Ala Asp Ser Thr Asn  
 50 55 60

30

Ser Gly Asp Asn Met Tyr Thr Leu Met Asn Ala Val Pro Pro Gly Pro  
 65 70 75 80

Asn

35

(2) INFORMATION FOR SEQ ID NO: 533:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Gly Pro Met Gly Gly Leu Gly Gly Met Glu Ser His His Met Asn Gly  
 1 5 10 15

50

Ser Leu Gly Ser Gly Asp Met Asp Ser Ile Ser Lys Asn Ser Pro Asn  
 20 25 30

Asn Met Ser Leu Ser Asn Gln Pro Gly Thr Pro Arg Asp Asp Gly Glu  
 35 40 45

55

Met Gly Gly Asn Phe Leu Asn Pro Phe Gln Ser Glu Ser Tyr Ser Pro  
 50 55 60

Ser Met Thr Met Ser Val  
 65 70

60

636

## (2) INFORMATION FOR SEQ ID NO: 534:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr  
1 5 10

15

## (2) INFORMATION FOR SEQ ID NO: 535:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

20 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Gln Ala Phe Val Leu Leu Ser Asp Leu Leu Leu Ile Phe Ser Pro Gln  
25 1 5 10 15

Met Ile Val Gly Gly Arg Asp Phe Leu Arg Pro Leu Val Phe Phe Pro  
20 25 30

30 Glu Ala Thr Leu Gln Ser Glu Leu Ala Ser Phe Leu Met Asp His Val  
35 40 45

Phe Ile Gln Pro Gly Asp Leu Gly Ser Gly Ala  
50 55

35

## (2) INFORMATION FOR SEQ ID NO: 536:

## 40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Ala Cys Ser Tyr Leu Leu Cys Asn Pro Glu Phe Thr Phe Phe Ser Arg  
1 5 10 15

50 Ala Asp Phe Ala Arg Ser Gln Leu Val Asp Leu Leu Thr Asp Arg Phe  
20 25 30

Gln Gln Glu Leu Glu Glu Leu Leu Gln Val Gly  
35 40

55

## (2) INFORMATION FOR SEQ ID NO: 537:

## 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

637

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

5 Gln Lys Gln Leu Ser Ser Leu Arg Asp Arg Met Val Ala Phe Cys Glu  
 1 5 10 15  
 Leu Cys Gln Ser Cys Leu Ser Asp Val Asp Thr Glu Ile Gln Glu Gln  
 20 25 30  
 10 Val Ser Thr  
 35

15

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

25 Gln Val Ile Leu Pro Ala Leu Thr Leu Val Tyr Phe Ser Ile Leu Trp  
 1 5 10 15  
 Thr Leu Thr His Ile Ser Lys Ser Asp Ala Ser  
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

40 Ser Thr His Asp Leu Thr Arg Trp Glu Leu Tyr Glu Pro Cys Cys Gln  
 1 5 10 15  
 Leu Leu Gln Lys Ala Val Asp Thr Gly Xaa Val Pro His Gln Val  
 20 25 30

45

(2) INFORMATION FOR SEQ ID NO: 540:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

55

Leu Ala Val Ser Thr Ser Phe Ile Cys Cys Ala Asp Ile Ser Thr Ala  
 1 5 10 15

60

Leu Pro Leu Gly Ser Ser Arg Pro Ala Pro Ala Pro Arg His Arg Glu  
 20 25 30

638

His Glu His Gly His Gln Ala Arg Pro Pro Arg Leu Leu Xaa Thr Ser  
           35                          40                          45

5 Leu Met Pro Leu Ser Thr Pro Ala Ala Ala Gln Leu Leu Trp Thr Gln  
       50                          55                          60

Leu Thr Pro Met Gly Gly Arg Pro Gly Gly Arg His Ser Pro Pro Thr  
   65                          70                          75                          80

10 Leu His Thr Gly Pro Arg Ala Leu Pro Pro Gly Pro Pro His Pro Ser  
                           85                          90                          95

15 Leu His Val Ala Ala Leu Ser Leu Leu Arg  
                           100                          105

(2) INFORMATION FOR SEQ ID NO: 541:

20 (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 207 amino acids

      (B) TYPE: amino acid

      (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Glu Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu  
   1                          5                          10                          15

30 Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly  
                           20                          25                          30

Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser  
                           35                          40                          45

35 Ser Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met  
                           50                          55                          60

Gln Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg  
   65                          70                          75                          80

Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile  
                           85                          90                          95

45 Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp  
                           100                          105                          110

Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr  
                           115                          120                          125

50 Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val  
                           130                          135                          140

Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu  
   145                          150                          155                          160

Arg Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe  
                           165                          170                          175

60 Gly Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met

639

180 185 190  
 Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser Ile Ile Gln Gly  
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 542:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

15

Ala Leu Leu Lys Tyr Arg Phe Phe Tyr Gln Phe Leu Leu Gly Asn Glu  
 1 5 10 15

20

Arg Ala Thr Ala Lys Glu Ile Arg Asp Glu Tyr Val Glu Thr Leu Ser  
 20 25 30

Lys Ile Tyr Leu Ser Tyr Tyr Arg Ser Tyr Leu Gly Arg Leu Met Lys  
 35 40 45

25

Val Gln Tyr Glu Glu Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu  
 50 55 60

Asp Thr Ala Lys Lys Gly Phe Xaa Ser Lys Pro Ser Leu Arg Ser Arg  
 65 70 75 80

30

Asn Thr Ile Phe Thr Leu Gly Thr Arg Gly Ser Val Ile Ser Pro Thr  
 85 90 95

35

Glu Leu Glu Ala Pro Ile Leu Val Pro His Thr Ala Gln Arg  
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 543:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Glu Gln Arg Tyr Pro Phe Glu Ala Leu Phe Arg Ser Gln His Tyr Xaa  
 1 5 10 15

50

Leu Leu Asp Asn Ser Cys Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe  
 20 25 30

Val Val Ser Gly Pro Xaa Ala His Asp Leu Phe His Ala Val Met Gly  
 35 40 45

55

Arg Thr Leu Ser Met Thr Leu Lys His Leu Asp Ser Tyr Leu Ala Asp  
 50 55 60

60

Cys Tyr Asp Ala Ile Ala Val Phe Leu Cys Ile His Ile Val Leu Arg  
 65 70 75 80

Val Gln Tyr Glu Glu Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu  
50 55 60

641

Asp Thr Ala Lys Lys Gly Phe Xaa Ser Lys Pro Ser Leu Arg Ser Arg  
 65 70 75 80  
 5 Asn Thr Ile Phe Thr Leu Gly Thr Arg Gly Ser Val Ile Ser Pro Thr  
 85 90 95  
 Glu Leu Glu Ala Pro Ile Leu Val Pro His Thr Ala Gln Arg Xaa Glu  
 100 105 110  
 10 Gln Arg Tyr Pro Phe Glu Ala Leu Phe Arg Ser Gln His Tyr Xaa Leu  
 115 120 125  
 Leu Asp Asn Ser Cys Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe Val  
 130 135 140  
 15 Val Ser Gly Pro Xaa Ala His Asp Leu Phe His Ala Val Met Gly Arg  
 145 150 155 160  
 20 Thr Leu Ser Met Thr Leu Lys His Leu Asp Ser Tyr Leu Ala Asp Cys  
 165 170 175  
 Tyr Asp Ala Ile Ala Val Phe Leu Cys Ile His Ile Val Leu Arg Phe  
 180 185 190  
 25 Arg Asn Ile Ala Ala Lys Arg Asp Val Pro Ala Leu Asp Arg Tyr Trp  
 195 200 205  
 Glu Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu  
 210 215 220  
 30 Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly  
 225 230 235 240  
 35 Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser  
 245 250 255  
 Ser Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Gln Arg Thr Met  
 260 265 270  
 40 Gln Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg  
 275 280 285  
 Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile  
 290 295 300  
 45 Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp  
 305 310 315 320  
 50 Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr  
 325 330 335  
 Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val  
 340 345 350  
 55 Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Gln Arg Gly Gln Ala Glu  
 355 360 365  
 60 Arg Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe  
 370 375 380

Gly Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met  
 385 390 395 400

5 Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser  
 405 410

10 (2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Tyr Glu Gly Lys Glu Phe Asp Tyr Val Phe Ser Ile Asp Val Asn Glu  
 1 5 10 15

Gly Gly Pro Ser Tyr Lys Leu Pro Tyr Asn Thr Ser Asp Asp Pro Trp  
 20 25 30

Leu Thr Ala Tyr Asn Phe Leu Gln Lys Asn Asp Leu Asn Pro Met Phe  
 25 35 40 45

Leu Asp Gln Val Ala Lys Phe Ile Ile Asp Asn Thr Lys Gly Gln Met  
 50 55 60

Leu Gly Leu Gly Asn Pro Ser Phe Ser Asp Pro Phe Thr Gly Gly Gly  
 30 65 70 75 80

Arg Tyr Val Pro Gly Ser Ser Gly Ser Ser Asn Thr Leu Pro Thr Ala  
 85 90 95

35 Asp Pro Phe Thr Gly Ala Gly Arg Tyr Val Pro Gly Ser Ala Ser Met  
 100 105 110

Gly Thr Thr Met Ala Gly Val Asp Pro Phe Thr Gly Asn Ser Ala Tyr  
 40 115 120 125

Arg Ser Ala Ala Ser Lys Thr Met Asn Ile Tyr Phe Pro Lys Lys Glu  
 130 135 140

45 Ala Val Thr Phe Asp Gln Ala Asn Pro Thr Gln Ile Leu Gly Lys Leu  
 145 150 155 160

Lys Glu Leu Asn Gly Thr Ala Pro Glu Glu Lys Lys Leu Thr Glu Asp  
 165 170 175

50 Asp Leu Ile Leu Leu Glu Lys Ile Leu Ser Leu Ile Cys Asn Ser Ser  
 180 185 190

Ser Glu Lys Pro Thr Val Gln Gln Leu Gln Ile Leu Trp Lys Ala Ile  
 55 195 200 205

Asn Cys Pro Glu Asp Ile Val Phe Pro Ala Leu Asp Ile Leu Arg Leu  
 210 215 220

60 Ser Ile Lys His Pro Ser Val Asn Glu Asn Phe Cys Asn Glu Lys Glu



225					230					235					240
Gly	Ala	Gln	Phe	Ser	Ser	His	Leu	Ile	Asn	Leu	Leu	Asn	Pro	Lys	Gly
				245					250					255	
Lys	Pro	Ala	Asn	Gln	Leu	Leu	Ala	Leu	Arg	Thr	Phe	Cys	Asn	Cys	Phe
			260					265					270		
Val	Gly	Gln	Ala	Gly	Gln	Lys	Leu	Met	Met	Ser	Gln	Arg	Glu	Ser	Leu
		275					280					285			
Met	Ser	His	Ala	Ile	Glu	Leu	Lys	Ser	Gly	Ser	Asn	Lys	Asn	Ile	
290						295					300				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Lys Asp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Ser

(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Leu Gly Val Asp Ser Gln Ile Lys Lys Tyr Ser Ser Val Ser Glu Pro  
 1 5 10 15  
 Ala Lys Val Ser Glu Cys Cys Arg Phe Ile Leu Asn Leu Leu  
 20 25 30

10

## (2) INFORMATION FOR SEQ ID NO: 551:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

20

Tyr Glu Gly Lys Glu Phe Asp Tyr Val Phe Ser Ile Asp Val Asn Glu  
 1 5 10 15  
 Gly Gly Pro Ser Tyr Lys Leu Pro Tyr Asn Thr Ser Asp Asp Pro Trp  
 20 25 30

25

Leu Thr Ala Tyr Asn Phe Leu Gln Lys Asn Asp Leu Asn Pro Met Phe  
 35 40 45

30

Leu Asp Gln Val Ala Lys Phe Ile Ile Asp Asn Thr Lys Gly Gln Met  
 50 55 60  
 Leu Gly Leu Gly Asn Pro Ser Phe Ser Asp Pro Phe Thr Gly Gly Gly  
 65 70 75 80

35

Arg Tyr Val Pro Gly Ser Ser Gly Ser Ser Asn Thr Leu Pro Thr Ala  
 85 90 95  
 Asp Pro Phe Thr Gly Ala Gly Arg Tyr Val Pro Gly Ser Ala Ser Met  
 100 105 110

40

Gly Thr Thr Met Ala Gly Val Asp Pro Phe Thr Gly Asn Ser Ala Tyr  
 115 120 125

45

Arg Ser Ala Ala Ser Lys Thr Met Asn Ile Tyr Phe Pro Lys Lys Glu  
 130 135 140  
 Ala Val Thr Phe Asp Gln Ala Asn Pro Thr Gln Ile Leu Gly Lys Leu  
 145 150 155 160

50

Lys Glu Leu Asn Gly Thr Ala Pro Glu Glu Lys Lys Leu Thr Glu Asp  
 165 170 175  
 Asp Leu Ile Leu Leu Glu Lys Ile Leu Ser Leu Ile Cys Asn Ser Ser  
 180 185 190

55

Ser Glu Lys Pro Thr Val Gln Gln Leu Gln Ile Leu Trp Lys Ala Ile  
 195 200 205

60

Asn Cys Pro Glu Asp Ile Val Phe Pro Ala Leu Asp Ile Leu Arg Leu  
 210 215 220

645

Ser Ile Lys His Pro Ser Val Asn Glu Asn Phe Cys Asn Glu Lys Glu  
 225 230 235 240  
 Gly Ala Gln Phe Ser Ser His Leu Ile Asn Leu Leu Asn Pro Lys Gly  
 5 245 250 255  
 Lys Pro Ala Asn Gln Leu Leu Ala Leu Arg Thr Phe Cys Asn Cys Phe  
 260 265 270  
 Val Gly Gln Ala Gly Gln Lys Leu Met Met Ser Gln Arg Glu Ser Leu  
 10 275 280 285  
 Met Ser His Ala Ile Glu Leu Lys Ser Gly Ser Asn Lys Asn Ile His  
 15 290 295 300  
 Ile Ala Leu Ala Thr Leu Ala Leu Asn Tyr Ser Val Cys Phe His Lys  
 305 310 315 320  
 Asp His Asn Ile Glu Gly Lys Ala Gln Cys Leu Ser Leu Ile Ser Thr  
 20 325 330 335  
 Ile Leu Glu Val Val Gln Asp Leu Glu Ala Thr Phe Arg Leu Leu Val  
 340 345 350  
 Ala Leu Gly Thr Leu Ile Ser Asp Asp Ser Asn Ala Val Gln Leu Ala  
 25 355 360 365  
 Lys Ser Leu Gly Val Asp Ser Gln Ile Lys Lys Tyr Ser Ser Val Ser  
 30 370 375 380  
 Glu Pro Ala Lys Val Ser Glu Cys Cys Arg Phe Ile Leu Asn Leu Leu  
 385 390 395 400

35

40 (2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu His Glu  
 1 5 10 15  
 His Ile Gln Arg Leu Ser Lys Val Val Thr Ala Asn His Arg Ala Leu  
 20 25 30  
 Gln Ile Pro Glu Val Tyr Leu Arg Glu Ala Pro Trp Pro Ser Ala Gln  
 35 40 45  
 Ser Glu Ile Arg Thr Ile Ser Ala Tyr Lys Thr Pro Arg Asp Lys Val  
 50 55 60  
 Gln Cys Ile Leu Arg Met Cys Ser Thr Ile Met Asn Leu Leu Ser Leu  
 60 65 70 75 80

646

Ala Asn Glu Asp Ser Val Pro Gly Ala Asp Asp Phe Val Pro Val Leu  
                             85                            90                            95

5 Val Phe Val Leu Ile Lys Ala Asn Pro Pro Cys Leu Leu Ser Thr Val  
                             100                            105                            110

Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys Leu Ser Gly Glu Glu Ser  
                             115                            120                            125

10 Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu  
                             130                            135

15

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

25

Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu His Glu  
   1                            5                            10                            15

His Ile Gln Arg Leu Ser Lys Val Val Thr Ala Asn His Arg Ala Leu  
                             20                            25                            30

30

Gln Ile Pro Glu Val Tyr Leu Arg Glu Ala Pro Trp Pro Ser Ala Gln  
                             35                            40                            45

Ser Glu Ile Arg Thr Ile Ser Ala Tyr Lys Thr Pro Arg Asp Lys Val  
                             50                            55                            60

35

Gln Cys Ile Leu Arg Met Cys Ser Thr Ile Met Asn Leu Leu Ser Leu  
                             65                            70                            75                            80

40

Ala Asn Glu Asp Ser Val Pro Gly Ala Asp Asp Phe Val Pro Val Leu  
                             85                            90                            95

Val Phe Val Leu Ile Lys Ala Asn Pro Pro Cys Leu Leu Ser Thr Val  
                             100                            105                            110

45

Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys Leu Ser Gly Glu Glu Ser  
                             115                            120                            125

Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu Phe Ile Lys Thr Ile  
                             130                            135                            140

50

55

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

60

(B) TYPE: amino acid

647

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

10 Glu Ala Pro Trp Pro Ser Ala Gln Ser Glu Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

20 Ser Gly Glu Glu Ser Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu  
1 5 10 15

35 Phe Ile Lys Thr Ile  
20

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

40 Ala Asp Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn  
1 5 10 15

50 Pro Pro

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

60

Tyr Lys Thr Pro Arg Asp Lys Val Gln Cys Ile Leu  
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 559:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

15

Gly Ala Asp Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys  
 1 5 10 15

20

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn Pro  
 1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 561:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

Ser Ala Arg Ala Ser Thr Gln Pro Pro Ala Gly Gln His Pro Gly Pro  
 1 5 10 15

45

Cys

50

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Pro Gly Arg Trp Arg Trp Gln Arg Asp Met His Pro Ala Arg Lys  
 1 5 10 15

60

Leu Leu Ser Leu Leu Phe Leu Ile Leu Met Gly Thr Glu Leu Thr Gln

20

25

30

Asp

5

(2) INFORMATION FOR SEQ ID NO: 563:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

15

Ser Ala Ala Pro Asp Ser Leu Leu Arg Ser Ser Lys Gly Ser Thr Arg  
1 5 10 15

20

Gly Ser Leu

25

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Ala Ala Ile Val Ile Trp Arg Gly Lys Ser Glu Ser Arg Ile Ala Lys  
1 5 10 15

35

Thr Pro Gly Ile  
20

40

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Pro Leu Gly Ile Thr Leu Pro Leu Gly Ala Pro Glu Thr Gly Gly Gly  
1 5 10 15

50

Asp

55

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

60

650

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Cys Ala Ala Glu Thr Trp Lys Gly Ser Gln Arg Ala Gly Gln Leu Cys  
1 5 10 15

Ala Leu Leu Ala  
20

10

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Phe Arg Gly Gly Gly Thr Leu Val Leu Pro Pro Thr His Thr Pro Glu  
1 5 10 15

Trp Leu Ile Leu  
20

25

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Arg Ser Ala Arg Pro Ser Leu Gly Cys Leu Pro Ser Trp Ala Phe  
1 5 10 15

Ser Gln Ala Leu Asn Ile  
20

40

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys  
1 5 10 15

55

Glu Lys Gly Asn Phe Asn  
20

60

(2) INFORMATION FOR SEQ ID NO: 570:



651

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu  
1 5 10 15  
Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg  
20 25

## (2) INFORMATION FOR SEQ ID NO: 571:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln  
1 5 10 15  
Arg Cys

## (2) INFORMATION FOR SEQ ID NO: 572:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala  
1 5 10 15  
Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp  
20 25 30  
Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn  
35 40

## (2) INFORMATION FOR SEQ ID NO: 573:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val  
1 5 10 15

652

Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr  
 20 25 30

5 Ser Gln Ala Gly Phe Ser Gly Glu Asp Arg Leu Glu Gln  
 35 40 45

10 (2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro  
 1 5 10 15

20

Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp  
 20 25 30

25

Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln  
 35 40 45

Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val  
 50 55 60

30

Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly  
 65 70 75 80

Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser  
 85 90

35

(2) INFORMATION FOR SEQ ID NO: 575:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys  
 1 5 10 15

50

Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr  
 20 25 30

Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu  
 35 40

55

(2) INFORMATION FOR SEQ ID NO: 576:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

653

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

5 Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile Val Lys Leu Ser Leu  
 1 5 10 15  
 Tyr Arg His Phe Thr Asn  
 20

10

(2) INFORMATION FOR SEQ ID NO: 577:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

20

Thr Leu Ile Leu Ala Val Ala Ala Ser Ile Val Phe Ile Ile Trp Thr  
 1 5 10 15  
 Thr Met Lys Phe Arg Ile  
 20

25

(2) INFORMATION FOR SEQ ID NO: 578:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Val Thr Cys Gln Ser Asp Trp Arg Glu Leu Trp Val Asp Asp Ala Ile  
 1 5 10 15  
 Trp Arg Leu Leu Phe Ser Met Ile Leu Phe Val Ile  
 20 25

40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe Ser  
 1 5 10 15  
 Pro Leu Ser Glu Glu Glu Glu Asp Glu Gln  
 20 25

55

60

654

## (2) INFORMATION FOR SEQ ID NO: 580:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe Ser  
1 5 10 15  
Pro Leu Ser Glu Glu Glu Glu Asp Glu Gln  
20 25

## (2) INFORMATION FOR SEQ ID NO: 581:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

Lys Glu Pro Met Leu Lys Glu Ser Phe Glu Gly Met Lys Met Arg Ser  
1 5 10 15  
Thr Lys Gln Glu Pro Asn Gly Asn Ser Lys Val Asn Lys Ala Gln Glu  
20 25 30  
Asp Asp Leu  
35

## (2) INFORMATION FOR SEQ ID NO: 582:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

Lys Trp Val Glu Glu Asn Val Pro Ser Ser Val Thr Asp Val Ala Leu  
1 5 10 15  
Pro Ala Leu Leu Asp Ser Asp Glu Glu Arg Met Ile Thr His Phe Glu  
20 25 30  
Arg Ser Lys Met Glu  
35

## (2) INFORMATION FOR SEQ ID NO: 583:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883:

Asp Pro Arg Val Arg Leu Asn Ser Leu Thr Cys Lys His Ile Phe Ile  
 1 5 11 18  
 Ser Leu Thr Gln  
 20

10

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884:

Tyr Glu Pro Met Asp Phe Asa Met Ala Leu Ile Tyr Asp  
 1 5 11

20

(2) INFORMATION FOR SEQ ID NO: 885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885:

Ile Arg His Glu Leu Thr Val Leu Arg Asp Thr Arg Pro Ala Cys Ala  
 1 5 11 18

30

(2) INFORMATION FOR SEQ ID NO: 886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886:

Met Asp Phe Asa Met Ala Leu Ile Tyr Arg  
 1 5 11

50

(2) INFORMATION FOR SEQ ID NO: 887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887:

60

656

Met Gln Glu Met Met Arg Asn Gln Asp Arg Ala Leu Ser Asn Leu Glu  
 1 5 10 15

Ser Ile Pro Gly Gly Tyr Asn Ala  
 20

10

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

Leu Arg Arg Met Tyr Thr Asp Ile Gln Glu Pro Met Leu Ser Ala Ala  
 1 5 10 15

20

Gln Glu Gln Phe Gly Gly Asn Pro Phe  
 20 25

25

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

Ala Ser Leu Val Ser Asn Thr Ser Ser Gly Glu Gly Ser Gln Pro Ser  
 1 5 10 15

35

Arg Thr Glu Asn Arg Asp Pro Leu Pro Asn Pro Trp Ala Pro Gln Thr  
 20 25 30

40

45

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Ser Gln Ser Ser Ser Ala Ser Ser Gly Thr Ala Ser Thr Val Gly Gly  
 1 5 10 15

55

Thr Thr Gly Ser Thr Ala Ser Gly Thr Ser Gly Gln Ser Thr Thr Ala  
 20 25 30

60

Pro Asn Leu Val Pro Gly Val Gly Ala Ser Met Phe Asn Thr Pro Gly  
 35 40 45

657

Met Gln Ser Leu Leu Gln Gln Ile Thr Glu Asn Pro Gln Leu Met Gln  
 50 55 60

5 Asn Met Leu Ser Ala Pro Tyr  
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro Asp Leu Ala Ala  
 1 5 10 15

20 Gln Met Met Leu Asn Asn Pro Leu Phe Ala Gly Asn Pro Gln Leu Gln  
 20 25 30

25 Glu Gln Met Arg Gln Gln Leu Pro Thr Phe Leu Gln Gln  
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 592:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala Met  
 1 5 10 15

40 Gln Ala Leu Leu Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr Glu  
 20 25 30

Ala Pro Gly Leu Ile Pro Gly Phe Thr Pro Gly Leu Gly Ala Leu Gly  
 35 40 45

45 Ser Thr Gly Gly Ser Ser Gly Thr Asn Gly Ser Asn Ala Thr Pro Ser  
 50 55 60

50 Glu Asn Thr Ser Pro Thr Ala Gly Thr  
 65 70

(2) INFORMATION FOR SEQ ID NO: 593:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

638

Thr Gln Pro Gly His Gln Gln Phe Ile Gln Gln Met Leu Gln Ala Leu  
 1 5 10 15  
 Ala Gly Val Asn Pro Gln Leu Gln Asn Pro Glu Val Arg Phe Gln Gln  
 5 20 25 30  
 Gln Leu Gln Gln Leu Ser Ala Met Gly Phe Leu Asn Arg Glu Ala Asn  
 35 40 45  
 Leu Gln Ala Leu Ile Ala Thr Gly Gly Asp Ile Asn Ala Ala Ile Glu  
 50 55 60  
 Arg Leu Leu Gly Ser Gln Pro Ser  
 65 70

15

(2) INFORMATION FOR SEQ ID NO: 594:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

25

Arg Asn Pro Ala Met Met Gln Glu Met Met Arg Asn Gln Asp Arg Ala  
 1 5 10 15

30

Leu Ser Asn Leu Glu Ser Ile Pro Gly Gly Tyr Asn Ala Leu Arg Arg  
 20 25 30

Met Tyr Thr Asp Ile Gln Glu Pro Met Leu Ser Ala Ala  
 35 40 45

35

(2) INFORMATION FOR SEQ ID NO: 595:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

45

Gly Asn Pro Phe Ala Ser Leu Val Ser Asn Thr Ser Ser  
 1 5 10

50

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids.

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

55

Glu Asn Arg Asp Pro Leu Pro Asn Pro Trp Ala  
 1 5 10

60



## (2) INFORMATION FOR SEQ ID NO: 597:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

Gly Lys Ile Leu Lys Asp Gln Asp Thr Leu Ser Gln His Gly Ile His  
1 5 10 15

15

Asp

20

## (2) INFORMATION FOR SEQ ID NO: 598:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

Gly Leu Thr Val His Leu Val Ile Lys Thr Gln Asn Arg Pro  
1 5 10

30

## (2) INFORMATION FOR SEQ ID NO: 599:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

40

Ser Glu Leu Gln Ser Gln Met Gln Arg Gln Leu Leu Ser Asn Pro Glu  
1 5 10 15

Met Met

45

## (2) INFORMATION FOR SEQ ID NO: 600:

50

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

Pro Glu Ile Ser His Met Leu Asn Asn Pro Asp Ile Met Arg  
1 5 10

60

## (2) INFORMATION FOR SEQ ID NO: 601:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

Arg Gln Leu Ile Met Ala Asn Pro Gln Met Gln Gln Leu Ile Gln Arg  
 1 5 10 15  
 Asn Pro

## (2) INFORMATION FOR SEQ ID NO: 602:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu  
 1 5 10 15  
 Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 603:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu Cys Leu Ala  
 1 5 10 15  
 Phe Val Glu Ser Lys Phe Asn  
 20

## (2) INFORMATION FOR SEQ ID NO: 604:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe Gln Ile Asn  
 1 5 10 15  
 Ser His Tyr Trp Cys Asn

20

## 5 (2) INFORMATION FOR SEQ ID NO: 605:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu  
1 5 10 15

15 Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser  
20 25

20

## (2) INFORMATION FOR SEQ ID NO: 606:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

30 Ile Arg Glu Val Asn Glu Val Ile Gln Asn Pro Ala Thr  
1 5 10

## 35 (2) INFORMATION FOR SEQ ID NO: 607:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

Ile Thr Arg Ile Leu Leu Ser His Phe Asn Trp Asp Lys Glu Lys Leu  
1 5 10 15

45 Met Glu Arg Tyr Phe Asp Gly Asn Leu Glu Lys Leu Phe Ala  
20 25 30

## 50 (2) INFORMATION FOR SEQ ID NO: 608:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

Asn Thr Arg Ser Ser Ala Gln Asp Met Pro Cys Gln Ile Cys Tyr Leu  
1 5 10 15

60

662

Asn Tyr Pro Asn Ser Tyr Phe  
20

5

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

15 Cys Asp Ile Leu Val Asp Asp Asn Thr Val Met Arg Leu Ile Thr Asp  
1 5 10 15

Ser Lys Val Lys Leu Lys Tyr Gln His Leu Ile Thr Asn Ser Phe Val  
20 25 30

20 Glu Cys Asn Arg Leu Leu Lys Trp Cys Pro Ala Pro Asp Cys His His  
35 40 45

Val Val Lys Val Gln Tyr Pro Asp Ala Lys Pro Val  
50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 610:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

35

Cys Asp Ile Leu Val Asp Asp Asn Thr Val Met Arg Leu Ile Thr Asp  
1 5 10 15

40 Ser Lys Val Lys Leu Lys Tyr Gln His Leu Ile Thr Asn Ser Phe Val  
20 25 30

Glu Cys Asn Arg Leu Leu Lys Trp Cys Pro Ala Pro Asp Cys His His  
35 40 45

45 Val Val Lys Val  
50

50

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Gly Cys Asn His Met Val Cys Arg Asn Gln Asn Cys Lys Ala Glu Phe  
1 5 10 15

60

663

Cys Trp Val Cys Leu Gly Pro Trp Glu Pro His Gly Ser Ala Trp Tyr  
20 25 30

5 Asn Cys Asn Arg Tyr Asn Glu Asp Asp Ala Lys Ala Ala Arg Asp Ala  
35 40 45

Gln Glu Arg Ser Arg Ala Ala Leu Gln Arg Tyr Leu  
50 55 60

10

(2) INFORMATION FOR SEQ ID NO: 612:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

20 Phe Tyr Cys Asn Arg Tyr Met Asn His Met Gln Ser Leu Arg Phe Glu  
1 5 10 15

His Lys Leu Tyr Ala Gln Val Lys Gln Lys Met Glu Glu Met Gln Gln  
20 25 30

25

His Asn Met Ser Trp Ile Glu Val Gln Phe Leu Lys Lys Ala Val Asp  
35 40 45

30 Val Leu Cys Gln Cys Arg Ala Thr Leu Met Tyr Thr  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 613:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

40

Tyr Val Phe Ala Phe Tyr Leu Lys Lys Asn Gln Ser Ile Ile Phe  
1 5 10 15

45 Glu Asn Asn Gln Ala Asp Leu Glu Asn Ala Thr Glu Val Leu Ser Gly  
20 25 30

Tyr Leu Glu Arg Asp Ile Ser Gln Asp Ser Leu Gln Asp Ile Lys Gln  
35 40 45

50

Lys Val Gln Asp Lys Tyr Arg Tyr Cys Glu Ser Arg  
50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

5 Thr Gly Leu Glu Cys Gly His Lys Phe Cys Met Gln Cys Trp Ser Glu  
 1 5 10 15  
 Tyr Leu Thr Thr Lys Ile Met Glu Glu Gly Met Gly Gln Thr Ile Ser  
 20 25 30  
 10 Cys Pro Ala His Gly  
 35

15 (2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

25 Met Trp Gly Tyr Leu Phe Val Asp Ala Ala Trp Asn Phe Leu Gly Cys  
 1 5 10 15  
 Leu Ile Cys Gly Trp  
 20

30 (2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

40 Met His Phe Ile Ser Ser Gly Asn Val Ser Ala Ile Arg Ser Ser Ile  
 1 5 10 15  
 Leu Leu Leu Arg Xaa Ser Leu Ser Tyr Leu Gly Asn Cys Leu Arg Val  
 20 25 30  
 45 Ser Ala Ile Phe Val Tyr Phe Leu Leu Phe Leu Leu Leu Ser  
 35 40 45

50 (2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

60 Met Asp Gln Ala Leu Arg Gly Ser Pro Ser Glu Gly Phe Ser Thr Asp  
 1 5 10 15

665

Pro Ser Pro Pro Gln Val Gly Arg Gln Ile Pro Ser Phe Pro Pro Trp  
 20 25 30

5 Arg Arg Leu Val Leu Pro Lys Ala Ser Gly Cys Phe Leu Glu Arg Glu  
 35 40 45

Trp Trp Leu Cys Val Phe Lys Leu Arg Thr Arg Pro Gly Ala Glu Ala  
 50 55 60

10 His Ala Tyr Asn Ser Ser Ile Leu Gly Gly Arg Gly Lys Gly Ile Thr  
 65 70 75 80

15

(2) INFORMATION FOR SEQ ID NO: 618:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

30

Met Leu Pro Ala Leu Ala Ser Cys Cys His Phe Ser Pro Pro Glu Gln  
 1 5 10 15

35

Ala Ala Arg Leu Lys Lys Leu Gln Glu Gln Glu Lys Gln Gln Lys Val  
 20 25 30

40

Glu Phe Arg Lys Arg Met Glu Lys Glu Val Ser Asp Phe Ile Gln Asp  
 35 40 45

45

Ser Gly Gln Ile Lys Lys Lys Phe Gln Pro Met Asn Lys Ile Glu Arg  
 50 55 60

50

Ser Ile Leu His Asp Val Val Glu Val Ala Gly Leu Thr Ser Phe Ser  
 65 70 75 80

55

Phe Gly Glu Asp Asp Cys Arg Tyr Val Met Ile Phe Lys Lys Glu  
 85 90 95

60

Phe Ala Pro Ser Asp Glu Glu Leu Asp Ser Tyr Arg Arg Gly Glu Glu  
 100 105 110

65

Trp Asp Pro Gln Lys Ala Glu Glu Lys Arg Asn Xaa Lys Glu Leu Ala  
 115 120 125

70

Gln Arg Gln  
 130

75

(2) INFORMATION FOR SEQ ID NO: 619:

80

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

666

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

5      Glu Glu Glu Ala Ala Gln Gln Gly Pro Val Val Val Ser Pro Ala Ser  
       1                  5                  10                  15  
     Asp Tyr Lys Asp Lys Tyr Ser His Leu Ile Gly Lys Gly Ala Ala Lys  
           20                  25                  30  
 10     Asp Ala Ala His Met Leu Gln Ala Asn Lys Thr Tyr Gly Cys Xaa Pro  
           35                  40                  45  
     Val Ala Asn Lys Arg Asp Thr Arg Ser Ile Glu Glu Ala Met Asn Glu  
           50                  55                  60  
 15     Ile Arg Ala Lys Lys Arg Leu Arg Gln Ser Gly Glu  
           65                  70                  75

## 20      (2) INFORMATION FOR SEQ ID NO: 620:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

30     Pro Pro Arg Arg Pro Ala Gln Leu Pro Leu Thr Pro Gly Ala Gly Gln  
       1                  5                  10                  15  
     Gly Ala Gly Arg Asp Lys Ala Ala Ala Ile Arg Ala His Pro Gly Ala  
           20                  25                  30  
 35     Pro Pro Leu Asn His Leu Leu Pro  
           35                  40

## 40      (2) INFORMATION FOR SEQ ID NO: 621:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

50     Ala Val Pro Gln Ala Gly Gly Lys Gln Val Phe Asp Leu Ser Pro Leu  
       1                  5                  10                  15  
     Glu Leu Gly Tyr Val Arg Gly Met Cys Val Cys Val  
           20                  25

## 55      (2) INFORMATION FOR SEQ ID NO: 622:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

5 Met Leu Pro Ala Leu Ala Ser Cys Cys His Phe Ser Pro Pro Glu Gln  
 1 5 10 15  
 Ala Ala Arg Leu Lys Lys Leu Gln Glu Gln Glu Lys Gln Gln Lys Val  
 20 25 30  
 10 Glu Phe Arg Lys Arg Met Glu Lys Glu Val Ser Asp Phe Ile Gln Asp  
 35 40 45  
 Ser Gly Gln Ile Lys Lys Lys Phe Gln Pro Met Asn Lys Ile Glu Arg  
 50 55 60  
 15 Ser Ile Leu His Asp Val Val Glu Val Ala Gly Leu Thr Ser Phe Ser  
 65 70 75 80  
 Phe Gly Glu Asp Asp Asp Cys Arg Tyr Val Met Ile Phe Lys Lys Glu  
 85 90 95  
 20 Phe Ala Pro Ser Asp Glu Glu Leu Asp Ser Tyr Arg Arg Gly Glu Glu  
 100 105 110  
 25 Trp Asp Pro Gln Lys Ala Glu Glu Lys Arg Asn Xaa Lys Glu Leu Ala  
 115 120 125  
 Gln Arg Gln Glu Glu Glu Ala Ala Gln Gln Gly Pro Val Val Val Ser  
 130 135 140  
 30 Pro Ala Ser Asp Tyr Lys Asp Lys Tyr Ser His Leu Ile Gly Lys Gly  
 145 150 155 160  
 Ala Ala Lys Asp Ala Ala His Met Leu Gln Ala Asn Lys Thr Tyr Gly  
 165 170 175  
 35 Cys Xaa Pro Val Ala Asn Lys Arg Asp Thr Arg Ser Ile Glu Glu Ala  
 180 185 190  
 40 Met Asn Glu Ile Arg Ala Lys Lys Arg Leu Arg Gln Ser Gly Glu  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 623:

45

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

55 Leu Leu Cys Pro Val Leu Asn Ser Gly Xaa Ser Trp Asn Phe Pro His  
 1 5 10 15  
 Pro Ser Gln Pro Glu Tyr Ser Phe His Gly Phe His Ser Thr Arg Leu  
 20 25 30  
 Trp Ile

60

## (2) INFORMATION FOR SEQ ID NO: 624:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

10

Pro Ser Thr Pro Trp Phe Leu Phe Leu Leu Gly Leu Thr Cys Pro Phe  
 1 5 10 15

15

Ser Thr Ser His Pro Arg Trp Asp Ser Ile Pro Pro  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 625:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu  
 1 5 10 15

30

Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu  
 20 25 30

Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys  
 35 40 45

35

Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser  
 50 55 60

40

Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu  
 65 70 75 80

Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr  
 85 90 95

45

Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp  
 100 105 110

Gly Ala Ser Ile Val Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala  
 115 120 125

50

Asp Arg Ser Thr Ser Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala  
 130 135 140

55

Met Ile Arg Pro Asp Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu  
 145 150 155 160

Leu His Cys Glu Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp  
 165 170 175

60

Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala

130 185 190

Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys  
195 200 205

5 Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn  
210 215 220

Val Asn Asp  
10 225

15 (2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu  
1 5 10 15

25 Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu  
20 25 30

Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys  
35 40 45

30 Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser  
50 55 60

35

40 (2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg Lys  
1 5 10 15

50 Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp Pro  
20 25 30

Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val Thr  
35 40 45

55 Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn His Glu Ser  
50 55 60

60 Leu  
65

## (2) INFORMATION FOR SEQ ID NO: 628:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu  
 1 5 10 15  
 Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro  
 20 25 30  
 Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly Arg Gly Asn Pro  
 35 40 45  
 Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu  
 50 55

## (2) INFORMATION FOR SEQ ID NO: 629:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Trp Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser  
 1 5 10 15  
 Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly  
 20 25 30  
 Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu  
 35 40 45  
 Asn Val Asn Asp  
 50

## (2) INFORMATION FOR SEQ ID NO: 630:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

Val Pro Glu Leu Pro Asp Arg Val His Gln Leu His Gln Ala Val Gln  
 1 5 10 15  
 Gly Cys Ala Leu Gly Arg Pro Gly Phe Pro Gly Gly Pro Thr His Ser  
 20 25 30

671

Gly His His Lys Ser His Pro Gly Pro Ala Gly Gly Asp Tyr Asn Arg  
                   35                  40                  45  
 5 Cys Asp Arg Pro Gly Gln Val His Leu His Asn Pro Arg Gly Thr Gly  
           50                  55                  60  
 Arg Arg Gly Gln Leu His Pro Thr Ala Gly Pro Gly Val His Arg Arg  
   65                  70                  75                  80  
 10 Ala Cys Pro Ser Gln Gln Leu Pro His Arg Leu Gly Pro Gly Val Pro  
                   85                  90                  95  
 Cys Pro Ser Pro Ser Leu Thr Pro Val Leu Pro Ser Trp Thr Gln Ser  
 15                  100                  105                  110  
 Trp Cys Gly Leu Pro Gly Tyr Thr Ser Ser Ser  
           115                  120

20

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 22 amino acids  
      (B) TYPE: amino acid  
      (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

30 Val His Gln Leu His Gln Ala Val Gln Gly Cys Ala Leu Gly Arg Pro  
    1                  5                  10                  15  
 Gly Phe Pro Gly Gly Pro  
                   20  
 35

(2) INFORMATION FOR SEQ ID NO: 632:

40 (i) SEQUENCE CHARACTERISTICS:  
      (A) LENGTH: 42 amino acids  
      (B) TYPE: amino acid  
      (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

45 Pro Thr His Ser Gly His His Lys Ser His Pro Gly Pro Ala Gly Gly  
    1                  5                  10                  15  
 50 Asp Tyr Asn Arg Cys Asp Arg Pro Gly Gln Val His Leu His Asn Pro  
           20                  25                  30  
 Arg Gly Thr Gly Arg Arg Gly Gln Leu His  
           35                  40  
 55

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:  
 60 (A) LENGTH: 55 amino acids

672

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

5 Leu His Pro Thr Ala Gly Pro Gly Val His Arg Arg Ala Cys Pro Ser  
 1 5 10 15  
 Gln Gln Leu Pro His Arg Leu Gly Pro Gly Val Pro Cys Pro Ser Pro  
 20 25 30  
 10 Ser Leu Thr Pro Val Leu Pro Ser Trp Thr Gln Ser Trp Cys Gly Leu  
 35 40 45  
 Pro Gly Tyr Thr Ser Ser Ser  
 15 50 55

(2) INFORMATION FOR SEQ ID NO: 634:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Ser Leu Arg Arg Pro Arg Ser Ala Ala Xaa Gln Thr Leu Thr Thr Phe  
 1 5 10 15  
 30 Leu Ser Ser Val Ser Ser Ala Ser Ser Ala Leu Pro Gly Ser Arg  
 20 25 30  
 Glu Pro Cys Asp Pro Arg Ala Pro Pro Pro Pro Arg Ser Gly Ser Ala  
 35 35 40 45  
 Ala Ser Cys Cys Ser Cys Cys Cys Ser Cys Pro Arg Arg Ala Pro  
 50 55 60  
 40 Leu Arg Ser Pro Arg Gly Ser Lys Arg Arg Ile Arg Gln Arg Glu Val  
 65 70 75 80  
 Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro  
 85 90 95  
 45 Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly  
 100 105 110  
 Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg  
 115 120 125  
 50 Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp  
 130 135 140  
 Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr  
 145 150 155 160  
 Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly  
 165 170 175  
 60 Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe

673

180 185 190

Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile  
195 200 205

5 Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile  
210 215 220

10 His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly  
225 230 235 240

Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys  
245 250 255

15 Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu  
260 265 270

Glu Leu Pro Lys  
275

20

(2) INFORMATION FOR SEQ ID NO: 635:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

Ser Leu Arg Arg Pro Arg Ser Ala Ala Xaa Gln Thr Leu Thr Thr Phe  
1 5 10 15

Leu Ser Ser Val Ser Ser Ala Ser Ser Ser Ala Leu Pro Gly Ser Arg  
20 25 30

Glu Pro Cys Asp Pro Arg Ala Pro Pro Pro Pro Arg Ser Gly Ser Ala  
35 40 45

40 Ala Ser Cys Cys Ser Cys Cys Cys Ser Cys Pro Arg Arg  
50 55 60

45 (2) INFORMATION FOR SEQ ID NO: 636:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Arg Ala Pro Leu Arg Ser Pro Arg Gly Ser Lys Arg Arg Ile Arg Gln  
1 5 10 15

Arg Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
20 25 30

60 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly  
35 40 45

Thr Pro Gly Ile  
50

5

(2) INFORMATION FOR SEQ ID NO: 637:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

15 Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu  
     1                    5                    10                    15  
 20 Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln  
                     20                    25                    30  
 Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala  
                     35                    40                    45  
 25 Glu Cys Thr Phe  
     50

30 (2) INFORMATION FOR SEQ ID NO: 638:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly  
     1                    5                    10                    15  
 40 Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe  
                     20                    25                    30  
 Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile  
                     35                    40                    45  
 45 Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile  
                     50                    55                    60  
 50 His Arg  
     65

55 (2) INFORMATION FOR SEQ ID NO: 639:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:



675

Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu  
 1 5 10 15  
 5 Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly  
 20 25 30  
 Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
 35 40 45  
 10 Leu Pro Lys  
 50  
 15  
 (2) INFORMATION FOR SEQ ID NO: 640:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:  
 Thr Lys Lys Glu Asn Cys Arg Pro Ala Ser Leu Met Asn Ile Asp Thr  
 1 5 10 15  
 Lys Ile Leu Asn Lys Ile Leu Met Asn Gln  
 20 25  
 30  
 (2) INFORMATION FOR SEQ ID NO: 641:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 214 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:  
 35 Met Cys Asn Leu Pro Ile Lys Val Val Cys Arg Ala Asn Ala Glu Tyr  
 1 5 10 15  
 Met Ser Pro Ser Gly Lys Val Pro Xaa Xaa His Val Gly Asn Gln Val  
 20 25 30  
 45 Val Ser Glu Leu Gly Pro Ile Val Gln Phe Val Lys Ala Lys Gly His  
 35 40 45  
 Ser Leu Ser Asp Gly Leu Glu Glu Val Gln Lys Ala Glu Met Lys Ala  
 50 50 55 60  
 Tyr Met Glu Leu Val Asn Asn Met Leu Leu Thr Ala Glu Leu Tyr Leu  
 65 70 75 80  
 55 Gln Trp Cys Asp Glu Ala Thr Val Gly Xaa Ile Thr His Xaa Arg Tyr  
 85 90 95  
 Gly Ser Pro Tyr Pro Trp Pro Leu Xaa His Ile Leu Ala Tyr Gln Lys  
 100 105 110  
 60

676

Gln Trp Glu Val Lys Arg Lys Xaa Lys Ala Ile Gly Trp Gly Lys Lys  
 115 120 125  
 5 Thr Leu Asp Gln Val Leu Glu Asp Val Asp Gln Cys Cys Gln Ala Leu  
 130 135 140  
 Ser Gln Arg Leu Gly Thr Gln Pro Tyr Phe Phe Asn Lys Gln Pro Thr  
 145 150 155 160  
 10 Glu Leu Asp Ala Leu Val Phe Gly His Leu Tyr Thr Ile Leu Thr Thr  
 165 170 175  
 Gln Leu Thr Asn Asp Glu Leu Ser Glu Lys Val Lys Asn Tyr Ser Asn  
 180 185 190  
 15 Leu Leu Ala Phe Cys Arg Arg Ile Glu Gln His Tyr Phe Glu Asp Arg  
 195 200 205  
 20 Gly Lys Gly Arg Leu Ser  
 210

25 (2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

Met Cys Asn Leu Pro Ile Lys Val Val Cys Arg Ala Asn Ala Glu Tyr  
 1 5 10 15  
 35 Met Ser Pro Ser Gly Lys Val Pro Xaa Xaa His Val Gly Asn Gln Val  
 20 25 30  
 Val Ser Glu Leu Gly Pro Ile Val Gln Phe Val Lys  
 35 40  
 40

(2) INFORMATION FOR SEQ ID NO: 643:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

Phe Val Lys Ala Lys Gly His Ser Leu Ser Asp Gly Leu Glu Glu Val  
 1 5 10 15  
 55 Gln Lys Ala Glu Met Lys Ala Tyr Met Glu Leu Val Asn Asn Met Leu  
 20 25 30  
 Leu Thr Ala Glu Leu Tyr Leu Gln Trp Cys Asp Glu  
 35 40  
 60

677

## (2) INFORMATION FOR SEQ ID NO: 644:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

5  
 10 Leu Gln Trp Cys Asp Glu Ala Thr Val Gly Xaa Ile Thr His Xaa Arg  
     1                    5                    10                    15  
 Tyr Gly Ser Pro Tyr Pro Trp Pro Leu Xaa His Ile Leu Ala Tyr Gln  
                     20                    25                    30  
 15 Lys Gln Trp Glu Val Lys Arg Lys Xaa Lys Ala Ile Gly Trp Gly Lys  
                     35                    40                    45  
 20 Lys Thr Leu  
     50

## (2) INFORMATION FOR SEQ ID NO: 645:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

25  
 30 Asp Gln Val Leu Glu Asp Val Asp Gln Cys Cys Gln Ala Leu Ser Gln  
     1                    5                    10                    15  
 35 Arg Leu Gly Thr Gln Pro Tyr Phe Phe Asn Lys Gln Pro Thr Glu Leu  
                     20                    25                    30  
 Asp Ala Leu Val Phe Gly His Leu Tyr Thr Ile  
                     35                    40

## (2) INFORMATION FOR SEQ ID NO: 646:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

45  
 50 Leu Thr Thr Gln Leu Thr Asn Asp Glu Leu Ser Glu Lys Val Lys Asn  
     1                    5                    10                    15  
 55 Tyr Ser Asn Leu Leu Ala Phe Cys Arg Arg Ile Glu Gln His Tyr Phe  
                     20                    25                    30  
 Glu Asp Arg Gly Lys Gly Arg Leu Ser  
                     35                    40

60

## (2) INFORMATION FOR SEQ ID NO: 647:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

5 Met Xaa Xaa Xaa Asn Ser His Ile Thr Ile Phe Thr Leu Asn Val Asn  
 1 5 10 15  
 Gly Leu Asn Ala Pro Asn Glu Arg His Arg Leu Ala Asn Trp Ile Gln  
 20 25 30  
 15 Ser Gln Asp Gln Val Cys Cys Ile Gln Glu Thr His Leu Thr Gly Arg  
 35 40 45  
 20 Asp Thr His Arg Leu Lys Ile Lys Gly Trp Arg Lys Ile Tyr Gln Ala  
 50 55 60  
 Asn Gly Lys Gln Lys Lys  
 65 70

25

## (2) INFORMATION FOR SEQ ID NO: 648:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

35 Phe Thr Leu Asn Val Asn Gly Leu Asn Ala Pro Asn Glu Arg His Arg  
 1 5 10 15  
 Leu Ala Asn Trp Ile Gln Ser Gln Asp Gln Val Cys  
 20 25

40

## (2) INFORMATION FOR SEQ ID NO: 649:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

50

Thr His Leu Thr Gly Arg Asp Thr His Arg Leu Lys Ile Lys Gly Trp  
 1 5 10 15

55

Arg

## (2) INFORMATION FOR SEQ ID NO: 650:

60

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

Gly Trp Arg Lys Ile Tyr Gln Ala Asn Gly Lys Gln Lys Lys  
 1 5 10

10

## (2) INFORMATION FOR SEQ ID NO: 651:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

Ile Tyr His Leu His Ser Trp Ile Phe Phe His Phe Lys Arg Ala Phe  
 1 5 10 15

Cys Met Cys Phe Ile Thr Met Lys Val Ile His Ala His Cys Ser Lys  
 20 25 30

25

Leu Arg Lys Cys Xaa Asn Ala Gln Ile Ser Val Phe Cys Thr Thr Leu  
 35 40 45

30

Thr Ala Ser Tyr Pro Thr  
 50

## (2) INFORMATION FOR SEQ ID NO: 652:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

Ile Tyr His Leu His Ser Trp Ile Phe Phe His Phe Lys Arg Ala Phe  
 1 5 10 15

45

Cys Met Cys Phe Ile Thr Met  
 20

50

## (2) INFORMATION FOR SEQ ID NO: 653:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

Lys Val Ile His Ala His Cys Ser Lys Leu Arg Lys Cys Xaa Asn Ala  
 1 5 10 15

60

680

Gln Ile Ser Val Phe Cys Thr Thr Leu Thr Ala Ser Tyr Pro Thr  
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

15

Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser Ile Leu  
 1 5 10 15

Pro Gly Leu Val Leu Ala Ser Cys Asp Gly Pro Ser Xaa Ser Gln Ala  
 20 25 30

20

Pro Ser Pro Trp Leu Thr Pro Asp Pro Ala Ser Val Gln Val Arg Leu  
 35 40 45

25

Leu Trp Asp Val Leu Thr Pro Asp Pro Asn  
 50 55

(2) INFORMATION FOR SEQ ID NO: 655:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

Gln Arg Gly Ile Tyr Arg Glu Ile Leu Phe Leu Thr Met Ala Ala Leu  
 1 5 10 15

40

Gly Lys Asp His Val Asp Ile Val Ala Phe Asp Lys Lys Tyr Lys Ser  
 20 25 30

Ala Phe Asn Lys Leu Ala Ser Ser Met Gly Lys Glu Glu Leu Arg His  
 35 40 45

45

Arg Arg Ala Gln Met Pro  
 50

50

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

60

Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser Ile Leu  
 1 5 10 15

681

Pro Gly Leu Val Leu Ala Ser  
20

5

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

15

Glu Asp Asp Gly Phe Asn Arg Ser Ile His Glu Val Ile Leu Lys Asn  
1 5 10 15

Ile Thr Trp Tyr Ser Glu Arg Val Leu Thr Glu Ile Ser Leu Gly Ser  
20 25 30

20

Leu Leu Ile Leu Val Val Ile Arg Thr Ile Gln Tyr Asn Met Thr Arg  
35 40 45

Thr Arg Asp Lys Tyr Leu His Thr Asn Cys Leu Ala Ala Leu Ala Asn  
50 55 60

25

Met Ser Ala Gln Phe Arg Ser Leu His Gln Tyr Ala Ala Gln Arg Ile  
65 70 75 80

30

Ile Ser Leu Phe Ser Leu Leu Ser Lys Lys His Asn Lys Val Leu Glu  
85 90 95

Gln Ala Thr Gln Ser Leu Arg Gly Ser Leu Ser Ser Asn Asp Val Pro  
100 105 110

35

Leu Pro Asp Tyr Ala Gln Asp Leu Asn Val Ile Glu Glu Val Ile Arg  
115 120 125

Met Met Leu Glu Ile Ile Asn Ser Cys Leu Thr Asn Ser Leu His His  
130 135 140

40

Asn Pro Asn Leu Val Tyr Ala Leu Leu Tyr Lys Arg Asp Leu Phe Glu  
145 150 155 160

45

Gln Phe Arg Thr His Pro Ser Phe Gln Asp Ile Met Gln Asn Ile Asp  
165 170 175

Leu Val Ile Ser Phe Phe Ser Ser Arg Leu Leu Gln Ala Gly Ser  
180 185 190

50

(2) INFORMATION FOR SEQ ID NO: 658:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

60

Glu Asp Asp Gly Phe Asn Arg Ser Ile His Glu Val Ile Leu Lys Asn

682

1                    5                    10                    15  
 Ile Thr Trp Tyr Ser Glu Arg Val Leu Thr Glu Ile Ser Leu Gly Ser  
                   20                    25                    30  
 5 Leu Leu Ile Leu Val Val  
                   35

10

(2) INFORMATION FOR SEQ ID NO: 659:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 53 amino acids  
 15       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

20 Arg Thr Ile Gln Tyr Asn Met Thr Arg Thr Arg Asp Lys Tyr Leu His  
    1                    5                    10                    15  
 Thr Asn Cys Leu Ala Ala Leu Ala Asn Met Ser Ala Gln Phe Arg Ser  
                   20                    25                    30  
 25 Leu His Gln Tyr Ala Ala Gln Arg Ile Ile Ser Leu Phe Ser Leu Leu  
                   35                    40                    45  
 Ser Lys Lys His Asn  
                   50

30

(2) INFORMATION FOR SEQ ID NO: 660:

35 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 56 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

40

Ser Cys Leu Thr Asn Ser Leu His His Asn Pro Asn Leu Val Tyr Ala  
    1                    5                    10                    15  
 45 Leu Leu Tyr Lys Arg Asp Leu Phe Glu Gln Phe Arg Thr His Pro Ser  
                   20                    25                    30  
 Phe Gln Asp Ile Met Gln Asn Ile Asp Leu Val Ile Ser Phe Phe Ser  
                   35                    40                    45  
 50 Ser Arg Leu Leu Gln Ala Gly Ser  
                   50                    55

55

(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 31 amino acids  
 60       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear



683

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

Lys Lys His Asn Lys Val Leu Glu Gln Ala Thr Gln Ser Leu Arg Gly  
 1 5 10 15  
 Ser Leu Ser Ser Asn Asp Val Pro Leu Pro Asp Tyr Ala Gln Asp  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO: 662:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile  
 1 5 10 15  
 Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys Glu Lys  
 20 25 30  
 Leu Pro Arg Val Thr Asn Lys Asn Ile Gly Leu Gly Phe Lys Asp Thr  
 35 40 45  
 Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe  
 50 55 60  
 Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr  
 65 70 75 80  
 Gln Asp Glu Asp Ala Glu Asp His Cys His Pro Pro Arg Leu Ser Ala  
 85 90 95  
 Leu His Pro Gln Val Gln Pro Leu Arg Glu Ala Pro Gln Glu His Val  
 100 105 110  
 Cys Thr Pro Val Pro Leu Leu Gln Gly Arg Pro Asp Arg  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO: 663:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

Met Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr  
 1 5 10 15  
 Ile Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val  
 20 25 30  
 His Leu Ser Pro Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr  
 35 40 45

684

Val Gly Gln Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu  
 50 55 60

5 Lys Val Thr Lys Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe  
 65 70 75

10 (1) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

15 (C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

Met Ala Asp Ile Gln Thr Gln Arg Ala Tyr Gln Lys Gln Pro Thr Ile  
 1 5 10 15

20 Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys  
 20 25 30

25 (1) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

30 (B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

Lys Leu Pro Arg Val Thr Asn Lys Asn Ile Gly Leu Gly Phe Lys Asp  
 1 5 10 15

Thr Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro  
 20 25 30

40 Phe Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val  
 35 40 45

Thr Gln Asp Glu Asp Ala Gln Asy His Cys  
 50 55

45 (1) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

His Cys His Pro Pro Arg Leu Ser Ala Leu His Pro Gln Val Gln Pro  
 1 5 10 15

60 Leu Arg Glu Ala Pro Gln Glu His Val Cys Thr Pro Val Pro Leu Leu  
 20 25 30

685

Gln Gly Arg Pro Asp Arg  
35

5

(2) INFORMATION FOR SEQ ID NO: 667:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

15 Met Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr  
1 5 10 15

Ile Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val  
20 25 30

20

His Leu Ser Pro  
35

25

(2) INFORMATION FOR SEQ ID NO: 668:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

35 Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr Val Gly Glu Cys  
1 5 10 15

Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Thr Lys  
20 25 30

40 Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe  
35 40

45. (2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

55 Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe  
1 5 10 15

Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr  
20 25 30

60 Gln

686

## (2) INFORMATION FOR SEQ ID NO: 670:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met  
 1 5 10 15  
 Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg  
 20 25 30  
 Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln Arg Ala Lys  
 35 40 45  
 Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly  
 50 55 60

## (2) INFORMATION FOR SEQ ID NO: 671:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

Thr Arg Met Ile Asp Leu Leu Glu Glu Tyr Met Val Tyr Arg Lys His  
 1 5 10 15  
 Thr Tyr Xaa Arg Leu Asp Gly Ser Ser Lys Ile Ser Glu Arg Arg Asp  
 20 25 30  
 Met Val Ala Asp Phe Gln Asn Arg Asn Asp Ile Phe Val Phe Leu Leu  
 35 40 45  
 Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala Xaa Asp Thr  
 50 55 60  
 Val His Phe  
 65

## (2) INFORMATION FOR SEQ ID NO: 672:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met  
 1 5 10 15

687

Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg  
 20 25 30

5

10 (2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

Val Tyr Arg Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln  
 1 5 10 15

20

Arg Ala Lys Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly  
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

Thr Arg Met Ile Asp Leu Leu Glu Glu Tyr Met Val Tyr Arg Lys His  
 1 5 10 15

35

Thr Tyr Xaa Arg Leu Asp Gly Ser Ser Lys Ile Ser Glu Arg Arg Asp  
 20 25 30

40

Met

45

(2) INFORMATION FOR SEQ ID NO: 675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

Arg Arg Asp Met Val Ala Asp Phe Gln Asn Arg Asn Asp Ile Phe Val  
 1 5 10 15

55

Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala  
 20 25 30

60

Xaa Asp Thr Val His Phe  
 35

688

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met  
1 5 10 15

Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg  
20 25 30

Leu Ile Cys Lys Gly  
35

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met  
1 5 10 15

Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg  
20 25 30

Leu Ile Cys Lys Gly  
35

(2) INFORMATION FOR SEQ ID NO: 678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

Arg Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln Arg Ala  
1 5 10 15

Lys Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly  
20 25

(2) INFORMATION FOR SEQ ID NO: 679:

(i) SEQUENCE CHARACTERISTICS:

689

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

5 Met Ser Leu His Gly Lys Arg Lys Glu Ile Tyr Lys Tyr Glu Ala Pro  
 1 5 10 15  
 10 Trp Thr Val Tyr Ala Met Asn Trp Ser Val Arg Pro Asp Lys Arg Phe  
 20 25 30  
 Arg Leu Ala Leu Gly Ser Phe Val Glu Glu Tyr Asn Asn Lys Val Gln  
 35 40 45  
 15 Leu Val Gly Leu Asp Glu Glu Ser Ser Glu Phe Ile Cys Arg Asn Thr  
 50 55 60  
 Phe Asp His Pro Tyr Pro Thr Thr Lys Leu Met Trp Ile Pro Asp Thr  
 65 70 75 80  
 20 Lys Gly Val Tyr Pro Asp Leu Leu Ala Thr Ser Gly Asp Tyr Leu Arg  
 85 90 95  
 25 Val Trp Arg Val Gly Glu Thr Glu Thr Arg Leu Glu Cys Leu Leu Asn  
 100 105 110  
 Asn Asn Lys Asn Ser Asp Phe Cys Ala Pro Leu Thr Ser Phe Asp Trp  
 115 120 125  
 30 Asn Glu Val Asp Pro Tyr Leu Leu Gly Thr Ser Ser Ile Asp Thr Thr  
 130 135 140  
 35 Cys Thr Ile Trp Gly Leu Glu Thr Gly Gln Val Leu Gly Arg Val Asn  
 145 150 155 160  
 Leu Val Ser Gly His Val Lys Thr Gln Leu Ile Ala His Asp Lys Glu  
 165 170 175  
 40 Val Tyr Asp Ile Ala Phe Ser Arg Ala Gly Gly Gly Arg Asp Met Phe  
 180 185 190  
 Ala Ser Val Gly Ala Asp Gly Ser Val Arg Met Phe Asp Leu Arg His  
 195 200 205  
 45 Leu Glu His Ser Thr Ile Ile Tyr Glu Asp Pro Gln His His Pro Leu  
 210 215 220  
 50 Leu Arg Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr Leu Ala Thr Met  
 225 230 235 240  
 Ala Met Asp Gly Met Glu Val Val Ile Leu Asp Val Arg Val Pro Ala  
 245 250 255  
 55 His Leu Xaa Pro Gly Thr Thr Ile Glu His Val Ser Met Ala Leu Leu  
 260 265 270  
 Gly Pro His Ile His Pro Ala Thr Ser Ala Leu Gln Arg Met Thr Thr  
 275 280 285  
 60 Arg Leu Ser Ser Gly Thr Ser Ser Lys Cys Pro Glu Pro Leu Arg Thr

690

290	295	300
Leu Ser Trp Pro Thr Gln Leu Xaa Gly Glu Ile Asn Asn Val Gln Trp 305 310 315 320		
Ala Ser Thr Gln Pro Glu Leu Ser Pro Ser Ala Thr Thr Thr Ala Trp 325 330 335		
Arg Tyr Ser Glu Cys Ser Val Gly Gly Ala Val Pro Thr Arg Gln Gly 340 345 350		
Leu Leu Tyr Phe Leu Pro Leu Pro His Pro Gln Ser 355 360		

15

(2) INFORMATION FOR SEQ ID NO: 680:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

25	Met Ser Leu His Gly Lys Arg Lys Glu Ile Tyr Lys Tyr Glu Ala Pro	1	5	10	15
	Trp Thr Val Tyr Ala Met Asn Trp Ser Val Arg Pro Asp Lys Arg Phe	20	25	30	
30	Arg Leu Ala Leu Gly Ser Phe Val Glu Glu Tyr Asn Asn Lys Val Gln	35	40	45	
	Leu Val Gly Leu Asp Glu Glu Ser Ser Glu Phe Ile Cys Arg Asn Thr	50	55	60	
35	Phe Asp His Pro Tyr Pro Thr Thr Lys Leu Met Trp Ile Pro Asp Thr	65	70	75	80
	Lys Gly Val Tyr Pro Asp Leu Leu Ala Thr Ser Gly Asp Tyr Leu Arg	85	90	95	
40	Val Trp Arg Val Gly Glu Thr Glu Thr Arg Leu Glu Cys Leu Leu Asn	100	105	110	
45	Asn Asn Lys Asn Ser Asp Phe Cys Ala Pro Leu Thr Ser Phe Asp Trp	115	120	125	
	Asn Glu Val Asp Pro Tyr Leu Leu	130	135		
50					

55 (2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:



691

Ser Phe Asp Trp Asn Glu Val Asp Pro Tyr Leu Leu Gly Thr Ser Ser  
 1 5 10 15

5 Ile Asp Thr Thr Cys Thr Ile Trp Gly Leu Glu Thr Gly Gln Val Leu  
 20 25 30

Gly Arg Val Asn Leu Val Ser Gly His Val Lys Thr Gln Leu Ile Ala  
 35 40 45

10 His Asp Lys Glu Val Tyr Asp Ile Ala Phe Ser Arg Ala Gly Gly Gly  
 50 55 60

Arg Asp Met Phe Ala Ser Val Gly Ala Asp Gly Ser Val Arg Met Phe  
 15 65 70 75 80

Asp Leu Arg His Leu Glu His Ser Thr Ile Ile Tyr Glu Asp Pro Gln  
 85 90 95

20 His His Pro Leu Leu Arg Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr  
 100 105 110

Leu Ala Thr Met Ala Met Asp Gly Met Glu Val Val Ile Leu Asp Val  
 115 120 125

25 Arg Val Pro Ala His Leu Xaa Pro Gly Thr Thr Ile  
 130 135 140

30

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

40

Val Gly Ala Asp Gly Ser Val Arg Met Phe Asp Leu Arg His Leu Glu  
 1 5 10 15

His Ser Thr Ile Ile Tyr Glu Asp Pro Gln His His Pro Leu Leu Arg  
 20 25 30

45

Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr Leu Ala Thr Met Ala Met  
 35 40 45

50

Asp Gly Met Glu Val Val Ile Leu Asp Val Arg Val Pro Ala His Leu  
 50 55 60

Xaa Pro Gly Thr Thr Ile Glu His Val Ser Met Ala Leu Leu Gly Pro  
 65 70 75 80

55

His Ile His Pro Ala Thr Ser Ala Leu Gln Arg Met Thr Thr Arg Leu  
 85 90 95

Ser Ser Gly Thr Ser Ser Lys Cys Pro Glu Pro Leu Arg Thr Leu Ser  
 100 105 110

60

Trp Pro Thr Gln Leu Xaa Gly Glu Ile Asn Asn Val Gln Trp Ala Ser

692

115 120 125

Thr Gln Pro Glu Leu Ser Pro Ser Ala Thr Thr Thr Ala Trp Arg Tyr  
130 135 140

5 Ser Glu Cys Ser Val Gly Gly Ala Val Pro Thr Arg Gln Gly Leu Leu  
145 150 155 160

10 Tyr Phe Leu Pro Leu Pro His Pro Gln Ser  
165 170

(2) INFORMATION FOR SEQ ID NO: 683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:

Leu Tyr Ala Thr Ala Thr Val Ile Ser Ser Pro Ser Thr Glu Xaa Leu  
1 5 10 15

25 Ser Gln Asp Gln Gly Asp Arg Ala Ser Leu Asp Ala Ala Asp Ser Gly  
20 25 30

Arg Gly Ser Trp Thr Ser Cys Ser Ser Gly Ser His Asp Asn Ile Gln  
35 40 45

30 Thr Ile Gln His Gln Arg Ser Trp Glu Thr Leu Pro Phe Gly His Thr  
50 55 60

35 His Phe Asp Tyr Ser Gly Asp Pro Ala Gly Leu Trp Ala Ser Ser Ser  
65 70 75 80

His Met Asp Gln Ile Met Phe Ser Asp His Ser Thr Lys Tyr Asn Arg  
85 90 95

40 Gln Asn Gln Ser Arg Glu Ser Leu Glu Gln Ala Gln Ser Arg Ala Ser  
100 105 110

Trp Ala Ser Ser Thr Gly Tyr Trp Gly Glu Asp Ser Glu Gly Asp Thr  
115 120 125

45 Gly Thr Ile Lys Arg Arg Gly Gly Lys Asp Val Ser Ile Glu Ala Glu  
130 135 140

50 Ser Ser Ser Leu Thr Ser Val Thr Thr Glu Glu Thr Lys Pro Val Pro  
145 150 155 160

Met Pro Ala His Ile Ala Val Ala Ser Ser Thr Thr Lys Gly Leu Ile  
165 170 175

55 Ala Arg Lys Glu Gly Arg Tyr Arg Glu Pro Pro Pro Thr Pro Pro Gly  
180 185 190

Tyr Ile Gly Ile Pro Ile Thr Asp Phe Pro Glu Gly His Ser His Pro  
195 200 205

60

693

Ala Arg Lys Pro Pro Asp Tyr Asn Val Ala Leu Gln Arg Ser Arg Met  
210 215 220

5 Val Ala Arg Ser Ser Asp Thr Ala Gly Pro Ser Ser Val Gln Gln Pro  
225 230 235 240

His Gly His Pro Thr Ser Ser Arg Pro Val Asn Lys Pro Gln Trp His  
245 250 255

10 Lys Xaa Asn Glu Ser Asp Pro Arg Leu Ala Pro Tyr Gln Ser Gln Gly  
260 265 270

15 Phe Ser Thr Glu Glu Asp Glu Asp Glu Gln Val Ser Ala Val  
275 280 285

(2) INFORMATION FOR SEQ ID NO: 684:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

His Met Asp Gln Ile Met Phe Ser Asp His Ser Thr Lys Tyr Asn Arg  
1 5 10 15

30 Gln Asn Gln Ser Arg Glu Ser Leu Glu Gln Ala Gln Ser Arg Ala Ser  
20 25 30

Trp Ala Ser Ser Thr Gly Tyr Trp Gly Glu  
35 40

35

(2) INFORMATION FOR SEQ ID NO: 685:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

45 Ser Val Thr Thr Glu Glu Thr Lys Pro Val Pro Met Pro Ala His Ile  
1 5 10 15

Ala Val Ala Ser Ser Thr Thr Lys Gly Leu Ile Ala Arg Lys Glu Gly  
20 25 30

50

Arg Tyr Arg Glu Pro Pro Pro Thr Pro Pro Gly Tyr Ile Gly Ile Pro  
35 40 45

Ile Thr Asp  
55 50

60 (2) INFORMATION FOR SEQ ID NO: 686:

694

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

5 Val Ala Leu Gln Arg Ser Arg Met Val Ala Arg Ser Ser Asp Thr Ala  
 1 5 10 15  
 10 Gly Pro Ser Ser Val Gln Gln Pro His Gly His Pro Thr Ser Ser Arg  
 20 25 30  
 15 Pro Val Asn Lys Pro Gln Trp His Lys Xaa Asn Glu Ser Asp Pro Arg  
 35 40 45  
 Leu Ala Pro Tyr Gln Ser Gln Gly Phe  
 50 55

20

## (2) INFORMATION FOR SEQ ID NO: 687:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

25 Cys Leu Leu Phe Val Phe Val Ser Leu Gly Met Arg Cys Leu Phe Trp  
 30 1 5 10 15  
 Thr Ile Val Tyr Asn Val Leu Tyr Leu Lys His Lys Cys Asn Thr Val  
 20 25 30  
 35 Leu Leu Cys Tyr His Leu Cys Ser Ile  
 35 40

40

## (2) INFORMATION FOR SEQ ID NO: 688:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

45 Ala Cys Ser Lys Leu Ile Pro Ala Phe Glu Met Val Met Arg Ala Lys  
 50 1 5 10 15  
 Asp Asn Val Tyr His Leu Asp Cys Phe Ala Cys Gln Leu Cys Asn Gln  
 20 25 30  
 55 Arg Xaa Cys Val Gly Asp Lys Phe Phe Leu Lys Asn Asn Xaa Xaa Leu  
 35 40 45  
 Cys Gln Thr Asp Tyr Gln Glu Gly Leu Met Lys Glu Gly Tyr Ala Pro  
 50 55 60  
 60 Xaa Val Arg

695

65

## 5 (2) INFORMATION FOR SEQ ID NO: 689:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

Ser Ala Leu Ser Glu Pro Gly Ala Pro Asp Arg Arg Arg Pro Cys Pro  
 1 5 10 15  
 Glu Ser Val Pro Arg Arg Pro Asp Asp Glu Gln Trp Pro Pro Pro Thr  
 20 25 30  
 Ala Leu Cys Leu Asp Val Ala Pro Leu Pro Pro Ser Ser  
 20 35 40 45

## 25 (2) INFORMATION FOR SEQ ID NO: 690:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu  
 1 5 10 15  
 Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly  
 35 20 25 30  
 Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile  
 40 35 40

## 45 (2) INFORMATION FOR SEQ ID NO: 691:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

Ala His Ala Ser Glu Ser Gly Glu Arg Trp Trp Ala Cys Cys Gly Val  
 1 5 10 15  
 Arg Phe Gly Leu Arg Ser Ile Glu Ala Ile Gly Arg Ser Cys Cys His  
 55 20 25 30  
 Asp Gly Pro Gly Gly Leu Val Ala Asn Arg Gly Arg Arg Phe Lys Trp  
 35 40 45  
 Ala Ile Glu Leu Ser Gly Pro Gly Gly Gly Ser Arg Gly Arg Ser Asp  
 60

696

50                      55                      60

Arg Gly Ser Gly Gln Gly Asp Ser Leu Tyr Pro Val Gly Tyr Leu Asp  
 65                      70                      75                      80

5 Lys Gln Val Pro Asp Thr Ser Val Gln Glu Thr Asp Arg Ile Leu Val  
                     85                      90                      95

10 Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly Pro Leu Lys Gln Ile Pro  
                     100                      105                      110

Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe  
                     115                      120                      125

15 Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu  
                     130                      135                      140

Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys  
                     145                      150                      155                      160

20 Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala  
                     165                      170                      175

25 Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala  
                     180                      185                      190

Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Phe Ser  
                     195                      200                      205

30 Gly Gly Gly Leu Leu Leu  
                     210

35 (2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys Phe Leu Gln Gly  
 1                      5                      10                      15

45 Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala Leu Ala Val Tyr  
                     20                      25                      30

Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala Ser Asp  
 50                      35                      40                      45

55 (2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

697

Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu  
1 5 10 15

5 Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly  
20 25 30

Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile  
35 40

10

(2) INFORMATION FOR SEQ ID NO: 694:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

20

Pro Thr Thr Lys Leu Asp Ile Met Glu Lys Lys Lys His Ile Gln Ile  
1 5 10 15

25

Arg Phe Pro Ser Phe Tyr His Lys Leu Val Asp Ser Gly Arg Met Arg  
20 25 30

Ser Lys Arg Glu Thr Arg Arg Glu Asp Ser Asp Thr Lys His Asn Leu  
35 40 45

30

35

(2) INFORMATION FOR SEQ ID NO: 695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

40

Thr Glu His Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys Asp  
1 5 10 15

45

Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln Met Thr Ile Ala  
20 25 30

50

Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg Gly Ser Leu Val  
35 40 45

Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp  
50 55 60

55

Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr Asn Ala Arg Asp  
65 70 75 80

Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys  
85 90 95

60

698

Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu Thr Asp Pro Asp  
                   100                  105                  110  
 5 Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr Lys Gln Asn Asp Val  
                   115                  120                  125  
 Val Arg Ile Leu Pro Cys Lys His Val Phe His Lys Ser Cys Val Asp  
                   130                  135                  140  
 10 Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met Cys Lys Leu Asn Ile  
                   145                  150                  155                  160  
 Leu Lys Ala Leu Gly Ile Val  
                                   165  
 15

(2) INFORMATION FOR SEQ ID NO: 696:

20 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 276 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:

Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr Glu  
   1                  5                  10                  15  
 30 Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val  
                   20                  25                  30  
 Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser  
                   35                  40                  45  
 35 Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile  
                   50                  55                  60  
 Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr  
   55                  70                  75                  80  
 40 Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys  
                   85                  90                  95  
 45 Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys  
                   100                  105                  110  
 Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr  
                   115                  120                  125  
 50 Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His  
                   130                  135                  140  
 Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met  
   145                  150                  155                  160  
 55 Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro  
                   165                  170                  175  
 60 Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln  
                   180                  185                  190



699

Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser  
 195 200 205

5 Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln  
 210 215 220

Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr  
 225 230 235 240

10 Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr  
 245 250 255

Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu  
 15 260 265 270

Val Glu Trp Phe  
 275

20

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

30 Thr Glu His Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys Asp  
 1 5 10 15

Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln Met Thr Ile Ala  
 20 25 30

35 Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg Gly Ser Leu Val  
 35 40 45

40 Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp  
 50 55 60

Leu Ile Phe Tyr Phe  
 65

45

(2) INFORMATION FOR SEQ ID NO: 698:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

50 Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp Leu Ile  
 1 5 10 15

Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr Asn Ala Arg Asp Arg Asn  
 20 25 30

60

700

Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys Leu Thr  
 35 40 45

5 Thr Arg Thr Val Lys Lys Gly Asp Lys Glu  
 50 55

(2) INFORMATION FOR SEQ ID NO: 699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

Val Lys Lys Gly Asp Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala  
 1 5 10 15

20 Val Cys Ile Glu Ser Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro  
 20 25 30

Cys Lys His Val Phe His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu  
 35 40 45

25 His Cys Thr Cys Pro Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly  
 50 55 60

30 Ile Val  
 65

(2) INFORMATION FOR SEQ ID NO: 700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr Glu  
 1 5 10 15

45 Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val  
 20 25 30

Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser  
 35 40 45

50 Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile  
 50 55 60

55 Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr  
 65 70 75 80

Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys  
 85 90 95

60 Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr

701

100

105

## 5 (2) INFORMATION FOR SEQ ID NO: 701:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

Ala Ala Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys  
 1 5 10 15

15

Gly Asp Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile  
 20 25 30

Glu Ser Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His  
 35 40 45

20

Val Phe His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr  
 50 55 60

Cys Pro Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro  
 65 70 75 80

25

Asn Leu Pro Cys

30

## (2) INFORMATION FOR SEQ ID NO: 702:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

Thr Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp  
 1 5 10 15

40

Asn Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu  
 20 25 30

45

Pro Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala  
 35 40 45

Val Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala  
 50 55 60

50

Leu Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala  
 65 70 75 80

55

Asn Glu Val Glu Trp Phe  
 85

60

702

## 2) INFORMATION FOR SEQ ID NO: 703:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

## (2) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

5                   Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg  
                   1                   5                   10                   15  
                  Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg  
                   20                   25                   30  
 15                  Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn  
                   35                   40                   45  
                  Ala Val Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val  
                   50                   55                   60  
 20                  Thr Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr  
                   65                   70                   75                   80  
                  Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser  
                   85                   90                   95  
                  Val Glu Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe  
                   100                   105                   110  
 30                  Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met  
                   115                   120                   125  
                  Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg  
                   130                   135                   140  
 35                  Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala  
                   145                   150                   155                   160  
                  Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp  
                   165                   170                   175  
                  Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser  
                   180                   185                   190  
 45                  Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe  
                   195                   200                   205  
                  His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro  
                   210                   215                   220  
 50                  Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu  
                   225                   230                   235                   240  
                  Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr  
                   245                   250                   255  
                  Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn  
                   260                   265                   270  
 60                  Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro

703

275                      280                      285

Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val  
 290                      295                      300

5 Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu  
 305                      310                      315                      320

10 Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn  
                                  325                      330                      335

Glu Val Glu Trp Phe  
                                  340

15

(2) INFORMATION FOR SEQ ID NO: 704:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

25 His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg Phe Phe  
     1                      5                      10                      15

Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn  
                                  20                      25                      30

30 Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn Ala Val  
                                  35                      40                      45

35 Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu  
     50                      55                      60

40

(2) INFORMATION FOR SEQ ID NO: 705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

45 Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile  
     1                      5                      10                      15

50 Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr  
                                  20                      25                      30

Phe Ile Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu  
                                  35                      40                      45

55 Gly Leu Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu  
     50                      55                      60

60 Glu Gly Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly  
     65                      70                      75                      80

704

	Glu	Glu	Pro	Arg	Ala	Gly	Lys	Glu	Glu	Ser	Gly	Val	Ser	Val	Ser	Asn	
	85							90							95		
5	Ser	Gln	Pro	Thr	Asn	Glu	Ser	His	Ser	Ile	Lys	Ala	Ile	Leu	Lys	Asn	
	100							105							110		
	Ile	Ser	Val	Leu	Ala	Phe	Ser	Val	Cys	Phe	Ile	Phe	Thr	Ile	Thr	Ile	
	115							120							125		
10	Gly	Met	Phe	Pro	Ala	Val	Thr	Val	Glu	Val	Lys	Ser	Ser	Ile	Ala	Gly	
	130							135							140		
15	Ser	Ser	Thr	Trp	Glu	Arg	Tyr	Phe	Ile	Pro	Val	Ser	Cys	Phe	Leu	Thr	
	145							150							155		
	Phe	Asn	Ile	Phe	Asp	Trp	Leu	Gly	Arg	Ser	Leu	Thr	Ala	Val	Phe	Met	
	165							170							175		
20	Trp	Pro	Gly	Lys	Asp	Ser	Arg	Trp	Leu	Pro	Ser	Trp	Xaa	Leu	Ala	Arg	
	180							185							190		
	Leu	Val	Phe	Val	Pro	Leu	Leu	Leu	Leu	Cys	Asn	Ile	Lys	Pro	Arg	Arg	
	195							200							205		
25	Tyr	Leu	Thr	Val	Val	Phe	Glu	His	Asp	Ala	Trp	Phe	Ile	Phe	Phe	Met	
	210							215							220		
30	Ala	Ala	Phe	Ala	Phe	Ser	Asn	Gly	Tyr	Leu	Ala	Ser	Leu	Cys	Met	Cys	
	225							230							235		
	Phe	Gly	Pro	Lys	Lys	Val	Lys	Pro	Ala	Glu	Ala	Glu	Thr	Ala	Glu	Pro	
	245							250							255		
35	Ser	Trp	Pro	Ser	Ser	Cys	Val	Trp	Val	Trp	His	Trp	Gly	Leu	Phe	Ser	
	260							265							270		
	Pro	Ser	Cys	Ser	Gly	Gln	Leu	Cys	Asp	Lys	Gly	Trp	Thr	Glu	Gly	Leu	
	275							280							285		
40	Pro	Ala	Ser	Leu	Pro	Val	Cys	Leu	Leu	Pro	Leu	Pro	Ser	Ala	Arg	Gly	
	290							295							300		
45	Asp	Pro	Glu	Trp	Ser	Gly	Gly	Phe	Phe	Phe							
	305							310									

(2) INFORMATION FOR SEQ ID NO: 706:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile  
1 5 10 15  
60 Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr

705

20 25 30

Phe Ile Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu  
35 40 45

5 Gly Leu Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu  
50 55 60

10 Glu Gly Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly  
65 70 75 80

Glu Glu Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn  
85 90 95

15 Ser Gln Pro Thr Asn Glu Ser His Ser Ile  
100 105

20 (2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 amino acids  
(B) TYPE: amino acid  
25 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

Ser Gly Val Ser Val Ser Asn Ser Gln Pro Thr Asn Glu Ser His Ser  
1 5 10 15

30 Ile Lys Ala Ile Leu Lys Asn Ile Ser Val Leu Ala Phe Ser Val Cys  
20 25 30

Phe Ile Phe Thr Ile Thr Ile Gly Met Phe Pro Ala Val Thr Val Glu  
35 35 40 45

Val Lys Ser Ser Ile Ala Gly Ser Ser Thr Trp Glu Arg Tyr Phe Ile  
50 55 60

40 Pro Val Ser Cys Phe Leu Thr Phe Asn Ile Phe Asp Trp Leu Gly Arg  
65 70 75 80

Ser

45

(2) INFORMATION FOR SEQ ID NO: 708:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

Thr Ile Gly Met Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile  
1 5 10 15

60 Ala Gly Ser Ser Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe  
20 25 30

706

Leu Thr Phe Asn Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val  
 35 40 45

5 Phe Met Trp Pro Gly Lys Asp Ser Arg Trp Leu Pro Ser Trp Xaa Leu  
 50 55 60

Ala Arg Leu Val Phe Val Pro Leu Leu Leu Cys Asn Ile Lys Pro  
 65 70 75 80

10 Arg Arg Tyr Leu Thr Val Val Phe Glu His Asp Ala  
 85 90

15

(2) INFORMATION FOR SEQ ID NO: 709:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

20 Phe Gly Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Glu Pro  
 1 5 10 15

Ser Trp Pro Ser Ser Cys Val Trp Val Trp His Trp Gly Leu Phe Ser  
 20 25 30

30 Pro Ser Cys Ser Gly Gln Leu Cys Asp Lys Gly Trp Thr Glu Gly Leu  
 35 40 45

Pro Ala Ser Leu Pro Val Cys Leu Leu Pro Leu Pro Ser Ala Arg Gly  
 50 55 60

35 Asp Pro Glu Trp Ser Gly Gly Phe Phe Phe  
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

50 Asp Asp Asp Gly Phe Glu Ile Val Pro Ile Glu Asp Pro Ala Lys His  
 1 5 10 15

Arg Ile Leu Asp Pro Glu Gly Leu Ala Leu Gly Ala Val Ile Ala Ser  
 20 25 30

55 Ser Lys Lys Ala Lys Arg Asp Leu Ile Asp Asn Ser Phe Asn Arg Tyr  
 35 40 45

Thr Phe Asn Glu Asp Glu Gly Glu Leu Pro Glu Trp Phe Val Gln Glu  
 50 55 60

60



707

Glu Lys Gln His Arg Ile Arg Gln Leu Pro Val Gly Lys Lys Glu Val  
 65 70 75 80  
 5 Glu His Tyr Arg Lys Arg Trp Arg Glu Ile Asn Ala Arg Pro Ile Xaa  
 85 90 95  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 100 105 110  
 10 Leu Glu Gln Thr Arg Lys Lys Ala Glu Ala Val Val Asn Thr Val Asp  
 115 120 125  
 Ile Xaa Arg Thr Arg Glu Ser  
 130 135  
 15

(2) INFORMATION FOR SEQ ID NO: 711:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:  
 25 Asp Asp Asp Gly Phe Glu Ile Val Pro Ile Glu Asp Pro Ala Lys His  
 1 5 10 15  
 Arg Ile Leu Asp Pro Glu Gly Leu Ala Leu Gly Ala Val Ile Ala Ser  
 30 20 25 30  
 Ser Lys Lys Ala Lys Arg Asp Leu Ile Asp Asn Ser Phe Asn Arg Tyr  
 35 40 45  
 35 Thr Phe  
 50

40 (2) INFORMATION FOR SEQ ID NO: 712:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:  
 Lys Arg Trp Arg Glu Ile Asn Ala Arg Pro Ile Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 50 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Arg Lys Lys Ala Glu Ala Val Val Asn Thr Val Asp Ile Xaa Arg Thr  
 55 35 40 45  
 Arg Glu Ser  
 50  
 60

## (2) INFORMATION FOR SEQ ID NO: 713:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

5 Met Ile Lys Asp Lys Gly Arg Ala Arg Thr Ala Leu Thr Ser Ser Gln  
    1              5                  10                  15  
 Pro Ala His Leu Cys Pro Glu Asn Pro Leu Leu His Leu Lys Ala Ala  
               20                  25                  30  
 15 Val Lys Glu Lys Lys Arg Asn Lys Lys Lys Thr Ile Gly Ser Pro  
       35                  40                  45  
 20 Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala  
       50                  55                  60  
 Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly  
   65                  70                  75                  80  
 25 Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu  
               85                  90                  95  
 Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp  
               100                  105                  110  
 30 Pro Ala Gly Cys Val Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val  
       115                  120                  125  
 35 Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile  
       130                  135                  140  
 Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val Lys Tyr Cys Thr  
   145                  150                  155                  160  
 40 Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys  
               165                  170                  175  
 Tyr Met Lys Arg Leu Met Gln Gln Ser Val Glu Ser Val Trp Asn Met  
               180                  185                  190  
 45 Ala Phe Asp Phe Ile Leu Asp Asn Val Gln Val Val Leu Gln Gln Thr  
       195                  200                  205  
 50 Tyr Gly Ser Thr Leu Lys Val Thr  
       210                  215

## (2) INFORMATION FOR SEQ ID NO: 714:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

709

Met Ile Lys Asp Lys Gly Arg Ala Arg Thr Ala Leu Thr Ser Ser Gln  
 1 5 10 15  
 5 Pro Ala His Leu Cys Pro Glu Asn Pro Leu Leu His Leu Lys Ala Ala  
 20 25 30  
 Val Lys Glu Lys Lys Arg Asn Lys Lys Lys Lys Thr Ile Gly Ser Pro  
 35 40 45  
 10 Lys Arg Ile Gln  
 50

15

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

20 Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala  
 1 5 10 15  
 Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly  
 20 25 30  
 30 Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu  
 35 40 45  
 Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp  
 50 55 60  
 35 Pro Ala Gly Cys Val Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val  
 65 70 75 80  
 40 Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile  
 85 90 95  
 Ser Asp Pro Met  
 100

45

(2) INFORMATION FOR SEQ ID NO: 716:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

55 Thr Ile Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val Lys Tyr  
 1 5 10 15  
 Cys Thr Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp Leu Val  
 20 25 30  
 60

710

Ile Lys Tyr Met Lys Arg Leu Met Gln Gln Ser Val Glu Ser Val Trp  
 35 40 45

5 Asn Met Ala Phe Asp Phe Ile Leu Asp Asn Val Gln Val Val Leu Gln  
 50 55 60

Gln Thr Tyr Gly Ser Thr Leu Lys Val Thr  
 65 70

10

(2) INFORMATION FOR SEQ ID NO: 717:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

20 Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Asn Cys  
 1 5 10 15

Glu Pro

25

(2) INFORMATION FOR SEQ ID NO: 718:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

35

Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Asn Cys  
 1 5 10 15

Glu Pro

40

(2) INFORMATION FOR SEQ ID NO: 719:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

Pro Gln Pro Ser Asn Phe Pro Thr Thr Val Arg Asn Leu Pro Tyr Ser  
 1 5 10 15

55

Gly Ala Gly Ala Gln Pro Pro Pro Ser Asn Cys  
 20 25

60

(2) INFORMATION FOR SEQ ID NO: 720:

711

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

5 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile  
 1 5 10 15  
 10 Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe  
 20 25 30  
 15 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp  
 35 40 45  
 Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys  
 50 55 60  
 20 Ser Ala Pro Ala Cys His Ala Ser Asp Thr His Leu Leu Tyr Pro Ser  
 65 70 75 80  
 Thr Arg Ala Leu Cys Pro Ser Ile Phe Ala Trp Leu Val Ala Pro His  
 85 90 95  
 25 Ser Val Phe Arg Thr Asn Ala Pro Gly Pro Thr Pro Ser Ser Gln Ser  
 100 105 110  
 30 Ser Pro Val Phe Pro Val Phe Pro Val Ser Phe Met Ala Leu Ile Val  
 115 120 125  
 Cys Xaa Leu Val Cys Cys  
 130

35

## (2) INFORMATION FOR SEQ ID NO: 721:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

40 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile  
 1 5 10 15  
 50 Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe  
 20 25 30  
 55 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp  
 35 40 45  
 Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys  
 50 55 60  
 Ser Ala Pro Ala Cys His Ala  
 65 70

60

## (2) INFORMATION FOR SEQ ID NO: 722:

## (i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

10 Phe Ala Trp Leu Val Ala Pro His Ser Val Phe Arg Thr Asn Ala Pro  
 1 5 10 15  
 Gly Pro Thr Pro Ser Ser Gln Ser Ser Pro Val Phe Pro Val Phe Pro  
 20 25 30  
 15 Val Ser Phe Met Ala Leu Ile Val Cys Xaa Leu Val Cys Cys  
 35 40 45

20

## (2) INFORMATION FOR SEQ ID NO: 723:

## (i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

30 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile  
 1 5 10 15  
 Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe  
 20 25 30  
 35 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp  
 35 40 45  
 Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys  
 50 55 60  
 40 Ser Ala Pro Ala Cys His Ala Ser Asp Thr His Leu Leu Tyr Pro Ser  
 65 70 75 80  
 Thr Arg Ala Leu Cys Pro Ser Ile Phe Ala Trp Leu Val Ala Pro His  
 45 85 90 95  
 Ser Val Phe Arg Thr Asn Ala Pro Gly Pro Thr Pro Ser Ser Gln Ser  
 100 105 110  
 50 Ser Pro Val Phe Pro Val Phe Pro Val Ser Phe Met Ala Leu Ile Val  
 115 120 125  
 Cys Xaa Leu Val Cys Cys  
 130

55

## (2) INFORMATION FOR SEQ ID NO: 724:

60

## (i) SEQUENCE CHARACTERISTICS:

713

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

5 Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Ala Leu Leu Gly Ser Ala  
1 5 10 15

10 Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu  
20 25 30

His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn  
35 40 45

15 Trp His Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile  
50 55 60

Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu  
65 70 75 80

20 Leu Met Lys Ser Ile His Ala Gly Leu Asn Ala Val Ala Ala Ile Leu  
85 90 95

25 Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn  
100 105 110

Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala Val  
115 120 125

30 Ile Cys Tyr Leu Leu Gln Leu Leu Ser Gly Phe Ser Val Phe Leu Leu  
130 135 140

Pro Trp Ala Pro Leu Ser Leu Arg Ala Phe Leu Met Pro Ile His Val  
145 150 155 160

35 Tyr Ser Gly Ile Val Ile Phe Gly Thr Val Ile Ala Thr Ala Leu Met  
165 170 175

40 Gly Leu Thr Glu Lys Leu Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser  
180 185 190

Thr Phe Pro Pro Glu Gly Val Phe Val Asn Thr Leu Gly Leu Leu Ile  
195 200 205

45 Leu Val Phe Gly Ala Leu Ile Phe Trp Ile Val Thr Arg Pro Gln Trp  
210 215 220

Lys Arg Pro Lys Glu Pro Asn Ser Thr Ile Leu His Pro Asn Gly Gly  
225 230 235 240

50 Thr Glu Gln Gly Ala Arg Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn  
245 250 255

Met Asp Lys Ser Asp Ser Glu Leu Asn Ser Glu Val Ala Ala Arg Lys  
260 265 270

Arg Asn Leu Ala Leu Asp Glu Ala Gly Gln Arg Ser Thr Met  
275 280 285

60

## (2) INFORMATION FOR SEQ ID NO: 725:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

10 Pro Gly Arg Ala Gly Pro Ser Pro Gly Leu Ser Leu Gln Leu Pro Ala  
 1 5 10 15  
 Glu Pro Gly His Pro Ala Gly Asn Leu Ala Pro Leu Thr Ser Arg Pro  
 20 25 30  
 15 Gln Pro Leu Cys Arg Ile Pro Ala Val Pro Gly  
 35 40

## (2) INFORMATION FOR SEQ ID NO: 726:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

30 Met Lys Leu Leu Gly Glu Cys Ser Ser Ser Ile Asp Ser Val Lys Arg  
 1 5 10 15  
 Leu Glu His Lys Leu Lys Glu Glu Glu Glu Ser Leu Pro Gly Phe Val  
 20 25 30  
 35 Asn Leu His Ser Thr Glu Thr Gln Thr Ala Gly Val Ile Asp Arg Trp  
 35 40 45  
 Glu Leu Leu Gln Ala Gln Ala Leu Ser Lys Glu Leu Arg Met Lys Gln  
 50 55 60  
 40 Asn Leu Gln Lys Trp Gln Gln Phe Asn Ser Asp Leu Asn Ser Ile Trp  
 65 70 75 80  
 Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln Leu Gln Arg Leu  
 45 85 90 95  
 Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu Gln Ile Lys Lys Leu  
 100 105 110  
 50 Lys Glu Leu Gln Lys Ala Val Asp His Arg Lys Ala Ile Ile Leu Ser  
 115 120 125  
 Ile Asn Leu Cys Ser Pro Glu Phe Thr Gln Ala Asp Ser Lys Glu Ser  
 130 135 140  
 55 Arg Asp Leu Gln Asp Arg Leu Xaa Gln Met Asn Gly Arg Trp Asp Arg  
 145 150 155 160  
 Val Cys Ser Leu Leu Glu Glu Trp Arg Gly Leu Leu Gln Asp Ala Leu  
 60 165 170 175



715

Met Gln Cys Gln Gly Phe His Glu Met Ser His Gly Leu Leu Leu Met  
 180 185 190

5 Leu Glu Asn Ile Asp Arg Arg Lys Asn Glu Ile Val Pro Ile Asp Ser  
 195 200 205

Asn Leu Asp Ala Glu Ile Leu Gln Asp His His Lys Gln Leu Met Gln  
 210 215 220

10 Ile Lys His Glu Leu Leu Glu Ser Gln Leu Arg Val Ala Ser Leu Gln  
 225 230 235 240

Asp Met Ser Cys Gln Leu Leu Val Asn Ala Glu Gly Thr Asp Cys Leu  
 245 250 255

15 Glu Ala Lys Glu Lys Val His Val Ile Gly Asn Arg Leu Lys Leu Leu  
 260 265 270

20 Leu Lys Glu Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu Asp  
 275 280 285

Val Ser Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala Asp Glu  
 290 295 300

25 Leu Asp Thr Ser Gly Ser Val Ser Pro Xaa Ser Gly Arg Ser Thr Pro  
 305 310 315 320

Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu Ser Gln Pro Gly  
 325 330 335

30 Pro Ser Val Ser Ser Pro His Ser Arg Ser Thr Lys Gly Gly Ser Asp  
 340 345 350

35 Ser Ser Leu Ser Glu Pro Xaa Pro Gly Arg Ser Gly Arg Gly Phe Leu  
 355 360 365

Phe Arg Val Leu Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu  
 370 375 380

40 Leu Ile Gly Leu Ala Cys Leu Val Pro Met Ser Glu Glu Asp Tyr Ser  
 385 390 395 400

Cys Ala Leu Ser Asn Asn Phe Ala Arg Ser Phe His Pro Met Leu Arg  
 405 410 415

Tyr Thr Asn Gly Pro Pro Pro Leu  
 420

50

(2) INFORMATION FOR SEQ ID NO: 727:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

60 Met Lys Leu Leu Gly Glu Cys Ser Ser Ser Ile Asp Ser Val Lys Arg

716

1                      5                      10                      15  
 Leu Glu His Lys Leu Lys Glu Glu Glu Ser Leu Pro Gly Phe Val  
                     20                      25                      30  
 5 Asn Leu His Ser Thr Glu Thr Gln Thr Ala Gly Val Ile Asp Arg Trp  
                     35                      40                      45  
 10 Glu Leu Leu Gln Ala Gln Ala Leu Ser Lys Glu Leu Arg Met Lys Gln  
                     50                      55                      60  
 Asn Leu Gln Lys Trp Gln Gln Phe Asn Ser Asp Leu Asn Ser Ile Trp  
                     65                      70                      75                      80  
 15 Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln Leu Gln Arg Leu  
                     85                      90                      95  
 Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu Gln Ile Lys  
                     100                      105                      110  
 20

(2) INFORMATION FOR SEQ ID NO: 728:

25 (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 136 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:

Lys Leu Lys Glu Leu Gln Lys Ala Val Asp His Arg Lys Ala Ile Ile  
   1                      5                      10                      15  
 35 Leu Ser Ile Asn Leu Cys Ser Pro Glu Phe Thr Gln Ala Asp Ser Lys  
                     20                      25                      30  
 Glu Ser Arg Asp Leu Gln Asp Arg Leu Xaa Gln Met Asn Gly Arg Trp  
                     35                      40                      45  
 40 Asp Arg Val Cys Ser Leu Leu Glu Glu Trp Arg Gly Leu Leu Gln Asp  
                     50                      55                      60  
 Ala Leu Met Gln Cys Gln Gly Phe His Glu Met Ser His Gly Leu Leu  
                     65                      70                      75                      80  
 45 Leu Met Leu Glu Asn Ile Asp Arg Arg Lys Asn Glu Ile Val Pro Ile  
                     85                      90                      95  
 50 Asp Ser Asn Leu Asp Ala Glu Ile Leu Gln Asp His His Lys Gln Leu  
                     100                      105                      110  
 Met Gln Ile Lys His Glu Leu Leu Glu Ser Gln Leu Arg Val Ala Ser  
                     115                      120                      125  
 55 Leu Gln Asp Met Ser Cys Gln Leu  
                     130                      135

60 (2) INFORMATION FOR SEQ ID NO: 729:

717

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80  
 85  
 90  
 95  
 100  
 105

Gln Asp Met Ser Cys Gln Leu Leu Val Asn Ala Glu Gly Thr Asp Cys  
 Leu Glu Ala Lys Glu Lys Val His Val Ile Gly Asn Arg Leu Lys Leu  
 Leu Leu Lys Glu Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu  
 Asp Val Ser Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala Asp  
 Glu Leu Asp Thr Ser Gly Ser Val Ser Pro Xaa Ser Gly Arg Ser Thr  
 Pro Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu Ser Gln Pro  
 Gly Pro Ser Val Ser Ser Pro His Ser

## (2) INFORMATION FOR SEQ ID NO: 730:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

40  
 45  
 50  
 55  
 60  
 65  
 70

Asp Ser Ser Leu Ser Glu Pro Xaa Pro Gly Arg Ser Gly Arg Gly Phe  
 Leu Phe Arg Val Leu Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu  
 Leu Leu Ile Gly Leu Ala Cys Leu Val Pro Met Ser Glu Glu Asp Tyr  
 Ser Cys Ala Leu Ser Asn Asn Phe Ala Arg Ser Phe His Pro Met Leu  
 Arg Tyr Thr Asn Gly Pro Pro Pro Leu

## (2) INFORMATION FOR SEQ ID NO: 731:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

718

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

5 Met Lys Leu Leu Ile Cys Gly Asn Tyr Leu Ala Pro Ser His Ser Glu  
 1 5 10 15  
 Ser Ser Arg Arg Cys Cys Leu Leu Cys Phe Tyr Pro Leu Cys Leu Glu  
 20 25 30  
 10 Ile Asn Phe Gly Met Lys Val Phe Leu Ser Met Pro Phe Leu Val Leu  
 35 40 45  
 Phe Gln Ser Leu Ile Gln Glu Asp  
 50 55

15

(2) INFORMATION FOR SEQ ID NO: 732:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn Lys Tyr Asp  
 1 5 10 15  
 Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu Val Lys Leu Val  
 20 25 30  
 Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys Lys Asp His Gln Ser  
 35 40 45  
 35 Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu Phe Ser Asp Phe Met Lys  
 50 55 60  
 Trp Ser Ile Pro Ala Phe Leu Tyr Phe Leu Asp Asn Leu Ile Val Phe  
 65 70 75 80  
 40 Tyr Val Leu Ser Tyr Leu Gln Pro Ala Met Ala Val Ile Phe Ser Asn  
 85 90 95  
 Phe Ser Ile Ile Thr Thr Ala Leu Leu Phe Arg Ile Val Leu Lys Xaa  
 100 105 110  
 Arg Leu Asn Trp Ile Gln Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser  
 115 120 125  
 50 Ile Val Ala Leu Thr Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala  
 130 135 140  
 Gly Arg Gly Phe His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys  
 145 150 155 160  
 55 Leu Leu Phe Arg Asn Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys  
 165 170 175  
 Glu Trp Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe  
 180 185 190

60

719

Ser His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys  
 195 200 205

5 Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys Glu  
 210 215 220

Gly Asn Gln Leu Thr Glu Xaa Ile Phe Ile Gln Asn Ser Lys Leu Tyr  
 225 230 235 240

10 Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu Gln Arg Ser  
 245 250 255

15 Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr Gly His Ser  
 260 265 270

20 (2) INFORMATION FOR SEQ ID NO: 733:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 94 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

Asn Ser Val Pro Asn Leu Gln Thr Leu Ala Val Leu Thr Glu Ala Ile  
 1 5 10 15

30 Gly Pro Glu Pro Ala Ile Pro Arg Xaa Pro Arg Glu Pro Pro Val Ala  
 20 25 30

Thr Ser Thr Pro Ala Thr Pro Ser Ala Gly Pro Gln Pro Leu Pro Thr  
 35 40 45

35 Gly Thr Val Leu Val Pro Gly Gly Pro Ala Pro Pro Cys Leu Gly Glu  
 50 55 60

40 Ala Trp Ala Leu Leu Leu Pro Pro Cys Arg Pro Ser Leu Thr Ser Cys  
 65 70 75 80

Phe Trp Ser Pro Arg Pro Ser Pro Trp Lys Glu Thr Gly Val  
 85 90

45

(2) INFORMATION FOR SEQ ID NO: 734:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

55 Ala Leu Gln Leu Ala Phe Tyr Pro Asp Ala Val Glu Glu Trp Leu Glu  
 1 5 10 15

Glu Asn Val His Pro Ser Leu Gln Arg Leu Gln Xaa Leu Leu Gln Asp  
 20 25 30

60

720

Leu Ser Glu Val Ser Ala Pro Pro  
35 40

5

(2) INFORMATION FOR SEQ ID NO: 735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

10

15

Cys His Pro Pro Ala Leu Ala Gly Thr Leu Leu Arg Thr Pro Glu Gly  
1 5 10 15

Arg Ala His Ala Arg Gly Leu Leu Leu Glu Ala Gly Gly Ala  
20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

25

30

Gly Ser Ser Ser Thr Arg Ser Trp Phe Ser Thr Ser Ser Pro Gln Arg  
1 5 10 15

Ser Ala Ser Trp His Ser Gly Ala Pro Ser Cys Arg Ser Trp Arg Leu  
20 25 30

35

Pro Cys Ser Trp Leu Ser Thr Arg Met Pro Trp Arg Ser Gly Trp Arg  
35 40 45

40

Lys Thr Cys Thr Pro Ala Cys Ser Gly Cys Lys  
50 55

45

(2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

50

Met Arg Pro Asp Trp Lys Ala Gly Ala Gly Pro Gly Gly Pro Pro Gln  
1 5 10 15

55

Lys Pro Ala Pro Ser Ser Gln Arg Lys Pro Pro Ala Arg Pro Ser Ala  
20 25 30

Ala Ala Ala Ala Ile Ala Val Ala Ala Ala Glu Glu Glu Arg Arg Leu  
35 40 45

60

721

Arg Gln Arg Asn Arg Leu Arg Leu Glu Glu Asp Lys Pro Ala Val Glu  
 50 55 60  
 5 Arg Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp  
 65 70 75 80  
 Ala Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp  
 85 90 95  
 10 Ser Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro  
 100 105 110  
 Gln Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Glu Met  
 115 120 125  
 15 Val Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala  
 130 135 140  
 Ser Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu  
 145 150 155 160  
 Glu Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr  
 165 170 175  
 25 Lys Arg Lys Thr Ser Ser Asp Asp Glu Ser Glu Glu Asp Glu Asp Asp  
 180 185 190  
 Leu Leu Gln Arg Thr Gly Asn Phe Ile Ser Thr Ser Thr Ser Leu Pro  
 195 200 205  
 30 Arg Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg  
 210 215 220  
 Pro Thr Val Ala Arg Ile Ser Ile Cys Ala Val Pro Ser Arg Cys Thr  
 225 230 235 240  
 Asp Cys Asp Gly Cys Trp Asp  
 245

40

(2) INFORMATION FOR SEQ ID NO: 738:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

50

Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp Ala  
 1 5 10 15

55

Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp Ser  
 20 25 30

Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro Gln  
 35 40 45

60

Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Glu Met Val  
 50 55 60

722

Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala Ser  
 65 70 75 80  
 5 Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu Glu  
 85 90 95  
 Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr Lys  
 100 105 110  
 10 Arg Lys Thr Ser Ser Asp Asp Glu Ser Glu Glu Asp Glu Asp Asp Leu  
 115 120 125  
 Leu Gln Arg Thr Gly Asn Phe Ile Ser Thr Ser Thr Ser Leu Pro Arg  
 130 135 140  
 Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg Pro  
 145 150 155 160  
 20 Thr Val Ala Arg Ile Ser Ile Cys Ala Val Pro Ser Arg Cys Thr Asp  
 165 170 175  
 Cys Asp Gly Cys  
 180  
 25

(2) INFORMATION FOR SEQ ID NO: 739:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 218 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:

35 Leu Lys Glu Lys Ile Val Arg Ser Phe Glu Val Ser Pro Asp Gly Ser  
 1 5 10 15  
 40 Phe Leu Leu Ile Asn Gly Ile Ala Gly Tyr Leu His Leu Leu Ala Met  
 20 25 30  
 Lys Thr Lys Glu Leu Ile Gly Ser Met Lys Ile Asn Gly Arg Val Ala  
 35 40 45  
 45 Ala Ser Thr Phe Ser Ser Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly  
 50 55 60  
 50 Asp Gly Glu Val Tyr Val Trp Asp Val Asn Ser Arg Lys Cys Leu Asn  
 65 70 75 80  
 Arg Phe Val Asp Glu Gly Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser  
 85 90 95  
 55 Arg Asn Gly Gln Tyr Val Ala Cys Gly Ser Asn Cys Gly Val Val Asn  
 100 105 110  
 Ile Tyr Asn Gln Asp Ser Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile  
 115 120 125  
 60 Lys Ala Ile Met Asn Leu Val Thr Gly Val Thr Ser Leu Thr Phe Asn



723

130                      135                      140

Pro Thr Thr Glu Ile Leu Ala Ile Ala Ser Glu Lys Met Lys Glu Ala  
145                      150                      155                      160

5 Val Arg Leu Val His Leu Pro Ser Cys Thr Val Phe Ser Asn Phe Pro  
                    165                      170                      175

10 Val Ile Lys Asn Lys Asn Ile Ser His Val His Thr Met Asp Phe Ser  
                    180                      185                      190

Pro Arg Ser Gly Tyr Phe Ala Leu Gly Asn Glu Lys Gly Lys Ala Leu  
                    195                      200                      205

15 Met Tyr Arg Leu His His Tyr Ser Asp Phe  
                    210                      215

20 (2) INFORMATION FOR SEQ ID NO: 740:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 167 amino acids

        (B) TYPE: amino acid

25          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

Lys Ile Asn Gly Arg Val Ala Ala Ser Thr Phe Ser Ser Asp Ser Lys  
1                      5                      10                      15

30 Lys Val Tyr Ala Ser Ser Gly Asp Gly Glu Val Tyr Val Trp Asp Val  
                    20                      25                      30

Asn Ser Arg Lys Cys Leu Asn Arg Phe Val Asp Glu Gly Ser Leu Tyr  
35                      35                      40                      45

Gly Leu Ser Ile Ala Thr Ser Arg Asn Gly Gln Tyr Val Ala Cys Gly  
                    50                      55                      60

40 Ser Asn Cys Gly Val Val Asn Ile Tyr Asn Gln Asp Ser Cys Leu Gln  
                    65                      70                      75                      80

Glu Thr Asn Pro Lys Pro Ile Lys Ala Ile Met Asn Leu Val Thr Gly  
45                      85                      90                      95

Val Thr Ser Leu Thr Phe Asn Pro Thr Thr Glu Ile Leu Ala Ile Ala  
                    100                      105                      110

50 Ser Glu Lys Met Lys Glu Ala Val Arg Leu Val His Leu Pro Ser Cys  
                    115                      120                      125

Thr Val Phe Ser Asn Phe Pro Val Ile Lys Asn Lys Asn Ile Ser His  
                    130                      135                      140

55 Val His Thr Met Asp Phe Ser Pro Arg Ser Gly Tyr Phe Ala Leu Gly  
                    145                      150                      155                      160

Asn Glu Lys Gly Lys Ala Leu  
                    165

60

## (2) INFORMATION FOR SEQ ID NO: 741:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val  
 1 5 10 15  
 Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Leu His Ser  
 15 20 25 30  
 Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly  
 35 40 45  
 Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu  
 50 55 60  
 Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu  
 65 70 75 80  
 Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro  
 85 90 95  
 Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met  
 100 105 110  
 Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro  
 115 120 125  
 Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Ser Phe  
 130 135 140  
 Pro Ala Gly Ala Ala Arg Pro Asp Pro Ser Tyr Ala Cys Leu Thr Pro  
 145 150 155 160  
 Cys Asp Ala Pro Thr Ser Pro Ser Leu Ser Thr Arg Ser Val Arg Thr  
 165 170 175  
 Pro Thr Pro Ala Thr Ser Gln Thr Pro Trp Cys Val Pro Ala Cys Arg  
 180 185 190  
 Lys Gly Ala Arg Thr Pro Ala Arg Val Thr Pro Gly Ala Leu Trp Ser  
 195 200 205  
 Val Thr Ser Leu Phe Lys Ala Leu Ser Pro Gly Ala Arg Ile Arg Val  
 210 215 220  
 Arg Ser Pro Glu Ser Leu Val Ser Thr Arg Lys Ser Ala Asn Met Trp  
 225 230 235 240  
 Thr Gly Ser Arg Arg Arg  
 245

60

725

## (2) INFORMATION FOR SEQ ID NO: 742:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

5  
 10 Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Leu His Ser Gln Pro  
 1 5 10 15  
 Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr  
 20 25 30  
 15 Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro  
 35 40 45  
 Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly  
 50 55 60  
 20 Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe  
 65 70 75 80  
 25 Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val  
 85 90 95  
 Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr  
 100 105 110  
 30 Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Ser Phe Pro Ala  
 115 120 125  
 Gly Ala Ala Arg Pro Asp Pro Ser Tyr Ala Cys Leu Thr Pro Cys Asp  
 130 135 140  
 35 Ala Pro Thr Ser Pro Ser Leu Ser Thr Arg Ser Val Arg Thr Pro Thr  
 145 150 155 160  
 40 Pro Ala Thr Ser Gln Thr Pro Trp Cys Val Pro Ala Cys Arg Lys Gly  
 165 170 175  
 Ala Arg Thr Pro Ala Arg Val Thr Pro Gly Ala Leu Trp Ser Val Thr  
 180 185 190  
 45 Ser Leu Phe Lys Ala Leu Ser Pro Gly Ala Arg Ile Arg Val Arg Ser  
 195 200 205  
 Pro Glu Ser Leu Val Ser Thr Arg Lys Ser Ala Asn Met Trp Thr Gly  
 210 215 220  
 50 Ser Arg Arg Arg  
 225

## (2) INFORMATION FOR SEQ ID NO: 743:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

60

726

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

5 Cys Lys Leu His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr  
 1 5 10 15  
 Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr  
 20 25 30  
 10 Ala Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His  
 35 40 45  
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Gln  
 50 55 60  
 15 Ser Phe Pro His Pro Gly Phe Asn Asn Ser  
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

30 Val Leu Gln Gly Arg Tyr Phe Ser Pro Ile Leu Glu Met Arg Arg Leu  
 1 5 10 15  
 Arg Pro Glu Gly Xaa Xaa Asn Leu Pro Gly Gly Ser Arg Ala Gln Lys  
 20 25 30  
 35 Glu Pro Arg Gln Asp Leu Thr Leu Val Leu Trp Pro His Cys Pro His  
 35 40 45  
 Phe Ala Met Thr Arg Ser Tyr Val Pro Thr Lys Gln Cys Met Val Gln  
 50 55 60  
 40 Gly Ser Phe Tyr Cys Ile Phe Ile Phe Lys Gly Pro Val Gln Asn Trp  
 65 70 75 80

45

Cys

50

(2) INFORMATION FOR SEQ ID NO: 745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:

55 Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln  
 1 5 10 15  
 60 Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp

727

20 25 30

Phe Gly His Val Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp  
38 40 45

5 Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val  
51 55 60

10 Ile Val Leu Tyr Arg Gln Gln Glu Val Leu Asp Cys Asp Cys Asp Met  
65 70 75 80

Ala Ser Val His His Leu Leu Ser Gln Ile Pro Gln Asp Leu Pro Tyr  
85 90 95

15 Glu Thr Leu Ile Ser Arg Lys Glu Thr Phe Leu Phe Ser Phe Pro His  
100 105 110

Pro Asn Leu Leu Gly Arg Pro Leu Pro Asn Ser Lys Leu Arg Gly Arg  
115 120 125

20 Gln Pro Leu Leu Ser Lys Thr Leu Ser Trp His Gln Pro Ser Arg Gly  
130 135 140

25 Leu Ile Trp Cys Cys Gly Ser Gly Lys Arg Gly Leu Leu Arg Pro Glu  
145 150 155 160

Asp Arg Thr Lys Asp Val Leu Thr Lys Pro Arg Thr Asn Arg Phe Val  
165 170 175

30 Lys Leu Ala Val Met Gly Leu Thr Val Ala Leu Gly Ala Ala Ala Leu  
180 185 190

Ala Val Val Lys Ser Ala Leu Glu Trp Ala Pro Lys Phe Gln Leu Gln  
195 200 205

35 Leu Phe Pro  
210

40

(2) INFORMATION FOR SEQ ID NO: 746:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:

50

Cys Pro Gln Phe Phe Ile Pro Ala Thr Leu Pro Cys Pro Phe Val Phe  
1 5 10 15

Ala Phe Thr Ser Glu Ala Ser Ser Arg Ala Tyr Leu Thr Gln Arg Gly  
20 25 30

55

Pro Gly Gly Leu Ala Gln Asn Leu Met Pro Leu Pro Val Gly Phe Trp  
35 40 45

60

Met Gly Ser Leu Pro Pro Pro Trp Cys Trp Arg Lys Trp Val Ser Glu  
50 55 60

728

Ala Cys Ser Cys Phe Cys  
65 70

5

(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:

Gly Phe Gly Ser Val Ser Ala Ala Gly Arg Ser Gly Gly Thr Trp  
15 1 5 10 15

Gln Pro Val Gln  
20

20

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:

Pro Gly Gly Leu Ala Val Gly Ser Arg Trp Trp Ser Arg Ser Leu Thr  
30 1 5 10 15

35

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

45

Leu Glu Pro Ser Arg Gln Arg Arg Pro Arg Arg Arg Gly Gly Thr Ser  
1 5 10 15

50

Arg Pro Glu Thr Asp Gln Arg Ala Lys Cys Trp Arg Gln Leu  
20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750:

729

Val Cys Leu Arg Cys Gln Asn Arg Met Glu Asn  
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751:

15 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
 1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
 20 25 30

Ala Xaa Ala Gly Ala Phe Ser Pro Ala Ser Thr Thr Thr Thr Arg Arg  
 35 40 45

25 His Leu Ser Ser Arg Asn Arg Pro Glu Gly Lys Val Leu Glu Thr Val  
 50 55 60

Gly Val Phe Glu Val Pro Lys Gln Asn Gly Lys Tyr Glu Thr Gly Gln  
 65 70 75 80

30 Leu Phe Leu His Ser Ile Phe Gly Tyr Arg Gly Val Val Leu Phe Pro  
 85 90 95

Trp Gln Ala Arg Leu Xaa Asp Arg Asp Val Ala Ser Ala Ala Pro Glu  
 100 105 110

35 Lys Ala Glu Asn Pro Ala Gly His Gly Ser Lys Glu Val Lys Gly Lys  
 115 120 125

40 Thr His Thr Tyr Tyr Gln Val Leu Ile Asp Ala Arg Asp Cys Pro His  
 130 135 140

Ile Ser Gln Arg Ser Gln Thr Glu Ala Val Thr Phe Leu Ala Asn His  
 145 150 155 160

45 Asp Asp Ser Arg Ala Leu Tyr Ala Ile Pro Gly Leu Asp Tyr Val Ser  
 165 170 175

His Glu Asp Ile Leu Pro Tyr Thr Ser Thr Asp Gln Val Pro Ile Gln  
 180 185 190

50 His Glu Leu Phe Glu Arg Phe Leu Leu Tyr Asp Gln Thr Lys Ala Pro  
 195 200 205

Pro Phe Val Ala Arg Glu Thr Leu Arg Ala Trp Gln Glu Lys Asn His  
 210 215 220

Pro Trp Leu Glu Leu Ser Asp Val His Arg Glu Thr Thr Glu Asn Ile  
 225 230 235 240

60 Arg Val Thr Val Ile Pro Phe Tyr Met Gly Met Arg Glu Ala Gln Asn

730

245 250 255

Ser His Val Tyr Trp Trp Arg Tyr Cys Ile Arg Leu Glu Asn Leu Asp  
260 265 270

5 Ser Asp Val Val Gln Leu Arg Glu Arg His Trp Arg Ile Phe Ser Leu  
275 280 285

10 Ser Gly Thr Leu Glu Thr Val Arg Gly Arg Gly Val Val Gly Arg Glu  
290 295 300

Pro Val Leu Ser Lys Glu Gln Pro Ala Phe Gln Tyr Ser Ser His Val  
305 310 315 320

15 Ser Leu Gln Ala Ser Ser Gly His Met Trp Gly Thr Phe Arg Phe Glu  
325 330 335

Arg Pro Asp Gly Ser His Phe Asp Val Arg Ile Pro Pro Phe Ser Leu  
340 345 350

20 Glu Ser Asn Lys Asp Glu Lys Thr Pro Pro Ser Gly Leu His Trp  
355 360 365

25

(2) INFORMATION FOR SEQ ID NO: 752:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

35

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

40

Ala

45

(2) INFORMATION FOR SEQ ID NO: 753:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:

55

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

60

Ala



731

## (2) INFORMATION FOR SEQ ID NO: 754:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

Ala

## (2) INFORMATION FOR SEQ ID NO: 755:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

Ala

## (2) INFORMATION FOR SEQ ID NO: 756:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

Ala

732

## (2) INFORMATION FOR SEQ ID NO: 757:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:

Val Leu Glu Thr Val Gly Val Phe Glu Val Pro Lys Gln Asn Gly Lys  
1 5 10 15  
Tyr Glu Thr Gly Gln Leu Phe Leu His Ser Ile Phe Gly Tyr Arg Gly  
20 25 30  
Val Val Leu  
35

## (2) INFORMATION FOR SEQ ID NO: 758:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

Gly Leu Asp Tyr Val Ser His Glu Asp Ile Leu Pro Tyr Thr Ser Thr  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 759:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

Asp Val His Arg Glu Thr Thr Glu Asn Ile Arg Val Thr Val Ile Pro  
1 5 10 15  
Phe Tyr Met

## (2) INFORMATION FOR SEQ ID NO: 760:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

Trp Trp Arg Tyr Cys Ile Arg Leu Glu Asn Leu Asp Ser Asp Val Val

733

1                    5                    10                    15  
Gln Leu Arg Glu Arg  
                    20

5

(2) INFORMATION FOR SEQ ID NO: 761:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:

15

Pro Ala Phe Gln Tyr Ser Ser His Val Ser Leu Gln Ala Ser Ser Gly  
1                    5                    10                    15

20

His Met Trp Gly Thr Phe Arg Phe Glu Arg  
                    20                    25

(2) INFORMATION FOR SEQ ID NO: 762:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:

30

Ser Leu Cys Cys Pro Glu Gly Ala Glu Gly Cys  
1                    5                    10

35

(2) INFORMATION FOR SEQ ID NO: 763:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:

45

Gln Leu Lys Lys Thr His Tyr Asp Arg Pro Cys Pro  
1                    5                    10

50

(2) INFORMATION FOR SEQ ID NO: 764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764:

55

Gln Leu Lys Lys Thr His Tyr Asp Arg Pro Cys Pro  
1                    5                    10

60

734

## (2) INFORMATION FOR SEQ ID NO: 765:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:

Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu  
 1 5 10 15

15

Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
 20 25 30

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val  
 35 40 45

20

Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln  
 50 55 60

Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser  
 65 70 75 80

25

Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp Phe Asp Glu Gly  
 85 90 95

30

Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile  
 100 105 110

Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu  
 115 120 125

35

Gln Val Arg Gly Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp  
 130 135 140

Arg Thr Asp Val Asn Ile Arg Val Ile Arg Pro Pro Asn Met Ala Ala  
 145 150 155 160

40

Arg Trp Arg Phe Trp Cys Val Ser Val Thr  
 165 170

45

## (2) INFORMATION FOR SEQ ID NO: 766:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:

55

Met Val Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser  
 1 5 10 15

60

## (2) INFORMATION FOR SEQ ID NO: 767:

735

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767:

Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu  
 1 5 10 15

10

15 (2) INFORMATION FOR SEQ ID NO: 768:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
 1 5 10 15

25

Phe

30

(2) INFORMATION FOR SEQ ID NO: 769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met  
 1 5 10 15

40

Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala  
 20 25 30

45

Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala  
 35 40 45

Phe Thr Asn Arg Ile Phe Phe Ala  
 50 55

50

(2) INFORMATION FOR SEQ ID NO: 770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

60

736

Met Val Asp Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met  
 1 5 10 15

5 Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro  
 20 25 30

10 (2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771:

Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu  
 1 5 10 15

20 Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val  
 20 25 30

Ile Arg Pro Pro Asn  
 35

25

(2) INFORMATION FOR SEQ ID NO: 772:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:

Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu Ala Val Ile Gly Gly  
 1 5 10 15

40 Leu Val Tyr Leu Arg Arg Val Ile Trp Asn Phe Ser Leu Ile Lys Leu  
 20 25 30

Asp Gly Leu Leu Gln Leu Cys Val Leu Cys Leu Leu  
 35 40

45

(2) INFORMATION FOR SEQ ID NO: 773:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:

55 Asp Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp  
 1 5 10 15

Ser

60

737

## (2) INFORMATION FOR SEQ ID NO: 774:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:

Cys Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys Glu Ser  
 1 5 10 15

15

Lys Asn Leu Asn  
 20

20

## (2) INFORMATION FOR SEQ ID NO: 775:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:

Val Leu Leu Val Ser Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe  
 1 5 10 15

30

35

## (2) INFORMATION FOR SEQ ID NO: 776:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val  
 1 5 10 15

45

Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp  
 20 25 30

50

Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser  
 35 40 45

55

## (2) INFORMATION FOR SEQ ID NO: 777:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

60

738

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:

5 Pro Ala Ala Trp Asp Asp Lys Thr Asn Ile Lys Thr Val Cys Thr Tyr  
 1 5 10 15  
 Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala Leu Thr Asp Cys Gln  
 20 25 30  
 10 Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys Glu Ser Lys Asn  
 35 40 45  
 15 Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys Gly Ser Gly Asn Gly  
 50 55 60  
 Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val Leu Leu Val Ser Leu  
 65 70 75 80  
 20 Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe  
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val  
 1 5 10 15  
 35 Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp  
 20 25 30  
 40 Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser  
 35 40 45  
 Xaa Xaa Xaa Xaa Xaa Pro Ala Ala Trp Asp Asp Lys Thr Asn Ile Lys  
 50 55 60  
 45 Thr Val Cys Thr Tyr Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala  
 65 70 75 80  
 Leu Thr Asp Cys Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg  
 85 90 95  
 50 Lys Glu Ser Lys Asn Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys  
 100 105 110  
 55 Gly Ser Gly Asn Gly Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val  
 115 120 125  
 Leu Leu Val Ser Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe  
 130 135 140

60



## (2) INFORMATION FOR SEQ ID NO: 779:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:

10 Met Asn Ser Ala Ala Gly Phe Ser His Leu Asp Arg Arg Glu Arg Val  
     1                    5                    10                    15  
 Leu Lys Leu Gly Glu Ser Phe Glu Lys Gln Pro Arg Cys Ala Ser Thr  
                     20                    25                    30  
 15 Leu Cys

20

## (2) INFORMATION FOR SEQ ID NO: 780:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:

30 Thr Ile Tyr Pro Thr Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val  
     1                    5                    10                    15  
 Ser Ile Thr Glu Arg Ala Leu Lys Leu Val Ser Asp  
                     20                    25

35

## (2) INFORMATION FOR SEQ ID NO: 781:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:

45 Arg Ala Leu Lys Gly Val Leu Arg Val Gly Val Leu Ala Lys Gly Leu  
     1                    5                    10                    15  
 Leu Leu Arg Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys  
                     20                    25                    30

50

## (2) INFORMATION FOR SEQ ID NO: 782:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:

60

740

Ala Leu Ala Ala Leu Arg His Ala Lys Trp Phe Gln Ala Arg Ala Asn  
 1 5 10 15

5 Gly Leu Gln Ser Cys Val Ile Ile Ile Arg Ile Leu Arg Asp Leu Cys  
 20 25 30

Gln Arg Val Pro Thr Trp Ser  
 35

10

(2) INFORMATION FOR SEQ ID NO: 783:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:

20 Gly Asp Ala Leu Arg Arg Val Phe Glu Cys Ile Ser Ser Gly Ile Ile  
 1 5 10 15

Leu

25

(2) INFORMATION FOR SEQ ID NO: 784:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:

35

Leu Ala Phe Arg Gln Ile His Lys Val Leu Gly Met Asp Pro Leu Pro  
 1 5 10 15

40

(2) INFORMATION FOR SEQ ID NO: 785:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

50

Thr Ile Tyr Pro Thr Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val  
 1 5 10 15

55

Ser Ile Thr Glu Arg Ala Leu Lys Leu Val Ser Asp Ser Leu Ser Glu  
 20 25 30

His Glu Lys Asn Lys Asn Lys Glu Gly Asp Asp Lys Lys Glu Gly Gly  
 35 40 45

60

741

Lys Asp Arg Ala Leu Lys Gly Val Leu Arg Val Gly Val Leu Ala Lys  
 50 55 60

5 Gly Leu Leu Leu Arg Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys  
 65 70 75 80

Ser Glu Lys Pro Ser Lys Thr Leu Leu Ser Arg Ile Ala Glu Asn Leu  
 85 90 95

10 Pro Lys Gln Leu Ala Val Ile Ser Pro Glu Lys Tyr Asp Ile Lys Cys  
 100 105 110

Ala Val Ser Glu Ala Ala Ile Ile Leu Asn Ser Cys Val Glu Pro Lys  
 115 120 125

15 Met Gln Val Thr Ile Thr Leu Thr Ser Pro Ile Ile Arg Glu Glu Asn  
 130 135 140

20 Met Arg Glu Gly Asp Val Thr Ser Gly Met Val Lys Asp Pro Pro Asp  
 145 150 155 160

Val Leu Asp Arg Gln Lys Cys Leu Asp Ala Leu Ala Ala Leu Arg His  
 165 170 175

25 Ala Lys Trp Phe Gln Ala Arg Ala Asn Gly Leu Gln Ser Cys Val Ile  
 180 185 190

Ile Ile Arg Ile Leu Arg Asp Leu Cys Gln Arg Val Pro Thr Trp Ser  
 195 200 205

30 Asp Phe Pro Ser Trp Ala Met Glu Leu Leu Val Glu Lys Ala Ile Ser  
 210 215 220

35 Ser Ala Ser Ser Pro Gln Ser Pro Gly Asp Ala Leu Arg Arg Val Phe  
 225 230 235 240

Glu Cys Ile Ser Ser Gly Ile Ile Leu Lys Gly Ser Pro Gly Leu Leu  
 245 250 255

40 Asp Pro Cys Glu Lys Asp Pro Phe Asp Thr Leu Ala Thr Met Thr Asp  
 260 265 270

Gln Gln Arg Glu Asp Ile Thr Ser Ser Ala Gln Phe Ala Leu Arg Leu  
 275 280 285

45 Leu Ala Phe Arg Gln Ile His Lys Val Leu Gly Met Asp Pro Leu Pro  
 290 295 300

50 Gln Met Ser Gln Arg Phe Asn Ile His Asn Asn Arg Lys Arg Arg Arg  
 305 310 315 320

Asp Ser Asp Gly Val Asp Gly Phe Glu Ala Glu Gly Lys Lys Asp Lys  
 325 330 335

55 Lys Asp Tyr Asp Asn Phe  
 340

60 (2) INFORMATION FOR SEQ ID NO: 786:

742

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg  
 1 5 10 15  
 Lys Gln Glu Asp Asp Arg Asp Gly  
 20

## (2) INFORMATION FOR SEQ ID NO: 787:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:

Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro Tyr  
 1 5 10 15  
 Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO: 788:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:

Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala  
 1 5 10 15  
 Leu Ile Pro His Ser Asp Gln Arg Leu Arg Pro Gln Arg Thr Lys Gln  
 20 25 30  
 Tyr Val

## (2) INFORMATION FOR SEQ ID NO: 789:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:

Ala Arg Leu Asn Val Gly Arg Glu Ser Leu Lys Arg Glu Met Leu Lys  
 1 5 10 15

743

Ser Gln Gly Val Lys Val Ser Glu Ser Pro Met Gly Ala Arg His Ser  
20 25 30

5 Ser Trp Pro Glu Gly Ala Ala Phe Cys Lys Lys Val Gln Gly Ala Gln  
35 40 45

Met Gln Phe Pro Pro Arg Arg  
50 55

10

(2) INFORMATION FOR SEQ ID NO: 790:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:

20

Ala Arg Leu Asn Val Gly Arg Glu Ser Leu Lys Arg Glu Met Leu  
1 5 10 15

25

(2) INFORMATION FOR SEQ ID NO: 791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:

35

Leu Lys Ser Gln Gly Val Lys Val Ser Glu Ser Pro Met Gly Ala Arg  
1 5 10 15

His Ser Ser Trp  
20

40

(2) INFORMATION FOR SEQ ID NO: 792:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:

50

Ala Phe Cys Lys Lys Val Gln Gly Ala Gln Met Gln Phe Pro Pro Arg  
1 5 10 15

Arg

55

(2) INFORMATION FOR SEQ ID NO: 793:

60

(i) SEQUENCE CHARACTERISTICS:

741

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793:

Ala Phe Cys Lys Lys Val Gln Gly Ala Gln Met Gln Phe Pro Pro Arg  
 1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO: 794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:

Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val Ala Glu Ser Arg  
 1 5 10 15

Phe Asn Asp Ala Ala Tyr Tyr Tyr Trp Met Leu Ser Met Gln Cys Leu  
 20 25 30

Asp Ile Ala Gln Asp  
 35

(2) INFORMATION FOR SEQ ID NO: 795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:

Pro Ala Gln Lys Asp Thr Met Leu Gly Lys Phe Tyr His Phe Gln Arg  
 1 5 10 15

Leu Ala Glu Leu Tyr His Gly Tyr His Ala Ile His Arg His Thr Glu  
 20 25 30

Asp Pro

(2) INFORMATION FOR SEQ ID NO: 796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:

Leu Ala Lys Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His

745

1                      5                      10                      15  
 Ala Tyr Asp Lys Leu Arg Gly Leu Tyr Ile Pro  
                     20                      25

5

(2) INFORMATION FOR SEQ ID NO: 797:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:

15

Ala Arg Phe Gln Lys Ser Ile Glu Leu Gly Thr Leu Thr Ile Arg Ala  
                     1                      5                      10                      15

20

Lys Pro Phe His Asp Ser Glu Glu Leu Val Pro Leu Cys Tyr Arg Cys  
                     20                      25                      30

Ser Thr Asn Asn  
                     35

25

(2) INFORMATION FOR SEQ ID NO: 798:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798:

35

Pro Leu Leu Asn Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro  
                     1                      5                      10                      15

Phe Ile Phe Ser Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe  
                     20                      25                      30

40

Tyr Leu Glu Glu Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp  
                     35                      40                      45

45

Leu Glu Val Leu Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Cys  
                     50                      55                      60

Lys Gln Gln Leu Pro Asp Ser Cys Gly  
                     65                      70

50

(2) INFORMATION FOR SEQ ID NO: 799:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:

60

Met Pro Tyr Ala Gln Trp Leu Ala Glu Asn Asp Arg Phe Glu Glu Ala

746

1                    5                    10                    15  
Gln Lys Ala Phe His Lys Ala Gly Arg Gln Arg Glu Ala  
                  20                    25  
5

(2) INFORMATION FOR SEQ ID NO: 800:

10            (i) SEQUENCE CHARACTERISTICS:

              (A) LENGTH: 36 amino acids

              (B) TYPE: amino acid

              (D) TOPOLOGY: linear

15            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:

Phe Ser Val His Arg Pro Glu Thr Leu Phe Asn Ile Ser Arg Phe Leu  
1                    5                    10                    15

20            Leu His Ser Leu Pro Lys Asp Thr Pro Ser Gly Ile Ser Lys Val Lys  
                  20                    25                    30

Ile Leu Phe Thr  
                  35  
25



## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>161</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet</span>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>March 27, 1997</u>	Accession Number <u>97979</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet</span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application Specialist Indications	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer <p style="text-align: center;">04 JUN 1998</p>	Authorized officer

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page <u>162</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <u>---</u></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>April 4, 1997</u>	Accession Number <u>97974</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <u>---</u></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application by the receiving Office on <u>10/10/97</u> at <u>Manassas, Virginia</u></div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on: <u>10/10/97</u> at <u>Manassas, Virginia</u></div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>162</u> line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>May 29, 1997</u>	Accession Number <u>209080</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

  

<div style="text-align: center;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application <div style="text-align: center; font-size: small;">Permanent Address of the Applicant</div></div> <div style="padding: 5px;">Authorized officer <u>[Signature]</u></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on: <u>                    </u></div> <div style="padding: 5px;">Authorized officer <u>                    </u></div>
---	--

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>164</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit December 3, 1997	Accession Number 209511
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application G. Anton Smith Paternal Specialist MED 3076 703/205-0017	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer 04 JUN 1998	Authorized officer

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>167</u> . line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    April 4, 1997	Accession Number    97975
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" style="margin-right: 10px;" type="checkbox"/><span>This sheet was received with the international application</span></div> <div style="border-top: 1px solid black; padding-top: 10px;">Authorized officer <div style="font-size: 1.2em; margin-top: 20px;">04 JUN 1998</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input style="margin-right: 10px;" type="checkbox"/><span>This sheet was received by the International Bureau on:</span></div> <div style="border-top: 1px solid black; padding-top: 10px;">Authorized officer</div>
---	---

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>167</u> line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <u>—</u>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    May 29, 1997	Accession Number    209081
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <u>—</u>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <div style="text-align: center;">JUN 1998</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>
---	--

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>171</u> line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <u>—</u></span>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>April 4, 1997</u>	Accession Number <u>97976</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <u>—</u></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
For receiving Office use only	For International Bureau use only
<input checked="checked" type="checkbox"/> This sheet was received with the international application Specialist VERSIONS	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer  <b>04 JUN 1998</b>	Authorized officer

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>172</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <u>---</u></span>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>	
Date of deposit <u>April 4, 1997</u>	Accession Number <u>97977</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <u>---</u></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application <p style="text-align: center;">International Specialist PCT/US98/11422</p>	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer <p style="font-size: 1.2em;">04 JUN 1998</p>	Authorized officer



## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 172, line N/A	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet</span>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 29, 1997	Accession Number 209082
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet</span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
For receiving Office use only	
<input checked="" type="checkbox"/> This sheet was received with the international application	For international Bureau use only
Authorized officer 04 JUN 1998	<input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>176</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209007
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer <div style="font-size: 1.2em; font-weight: bold;">04 JUN 1998</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer</div>

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>176</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    May 29, 1997	Accession Number    209083
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received with the international application by the <u>receiving specialist</u> of the <u>receiving Office</u></div> <div style="padding: 5px;">Authorized officer: <u>[Signature]</u> <div style="text-align: center; font-weight: bold; font-size: 1.2em;">04 JUN 1998</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on: <u>                    </u></div> <div style="padding: 5px;">Authorized officer: <u>                    </u></div>
---	---

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>179</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209008
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">338</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
---	---

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>179</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet</span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    May 29, 1997	Accession Number    209084
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet</span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"><input type="checkbox"/> This sheet was received with the international application Specialist Operations</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer <div style="text-align: center; font-size: 1.2em;">JUN 1998</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer</div>

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>180</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209010
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	
<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"><input type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">APR 28 1998</div></div>	<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px;">Authorized officer</div>

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>180</u> line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    May 29, 1997	Accession Number    209085
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received with the international application <div style="text-align: center;">SECRET Operations</div></div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <div style="text-align: center; font-size: 1.2em;">04 JUN 1998</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>182</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209009
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>	<div style="text-align: center;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
--	---



## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>186</u> line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209011
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application by a Specialist in PCT Operations</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer <div style="font-size: 1.2em; margin-top: 10px;">04 JUN 1998</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer</div>
---	---

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>174</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>April 7, 1998</u>	Accession Number <u>209746</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	
For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer  <u>64 JUN 1998</u>	Authorized officer

*What Is Claimed Is:*

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15. A method of making an isolated polypeptide comprising:

- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
- (b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- (a) contacting the polypeptide of claim 11 with a binding partner; and
- (b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

## PATENT COOPERATION TREATY

## PCT

## DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a) and Rule 39)

Applicant's or agent's file reference PZ007PCT	IMPORTANT DECLARATION	Date of mailing (day/month/year) 14 OCT 1998
International application No. PCT/US98/11422	International filing date (day/month/year) 04 JUNE 1998	(Earliest) Priority Date (day/month/year) 06 JUNE 1997
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant HUMAN GENOME SCIENCES, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
- a. ☐ scientific theories.
  - b. ☐ mathematical theories.
  - c. ☐ plant varieties.
  - d. ☐ animal varieties.
  - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
  - f. ☐ schemes, rules or methods of doing business.
  - g. ☐ schemes, rules or methods of performing purely mental acts.
  - h. ☐ schemes, rules or methods of playing games.
  - i. ☐ methods for treatment of the human body by surgery or therapy.
  - j. ☐ methods for treatment of the animal body by surgery or therapy.
  - k. ☐ diagnostic methods practiced on the human or animal body.
  - l. ☐ mere presentations of information.
  - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out
- ☐ the description      ☐ the claims      ☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out
- ☒ it does not comply with the prescribed standard
- ☒ it is not in the prescribed machine readable form
4. Further comments:  
Please See Continuation Sheet.

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer <i>Brian R. Stanton</i> BRIAN R. STANTON
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

DECLARATION OF NON-ESTABLISHMENT OF  
INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/11422

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(6): A01N 37/18, 43/04; C12Q 1/00, 1/02, 1/68; C12N 5/00, 5/06, 15/00, 15/06, 15/09, 15/10, 15/11; G01N 33/53

US CL.: 435, 4, 7.1, 69.1, 70.1, 71.1, 172.3, 243, 320.1, 325, 410; 514/2, 44; 530/350, 387.1

4. Further Comments (Continued):

Applicant has not responded to the invitation to pay additional fees mailed on 04 August 1998. Therefore, the search would be conducted on the first appearing invention which includes claims 1-10, 14, and 15 in so far as these claims are drawn to the first ten (10) appearing nucleotide sequences. However, no meaningful search could be carried out on these sequences because the CRF that was received for this case on 15 June 1998 was technically defective and could not be used to conduct a search of the prior art.